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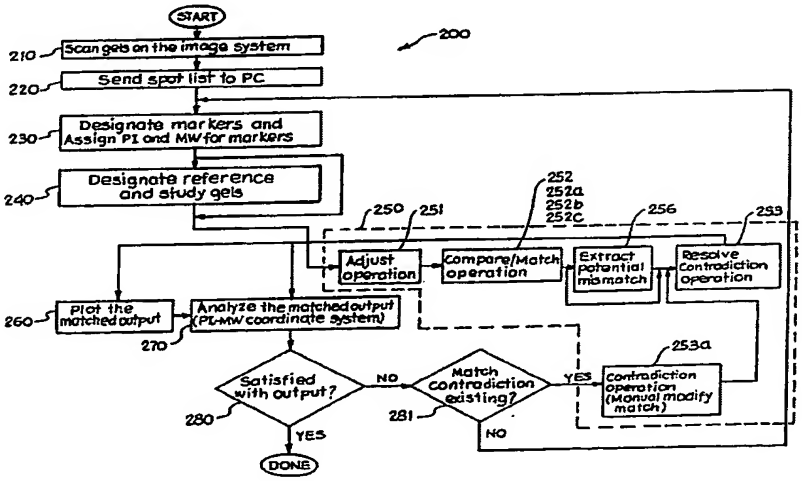
(54) Title: A COMPUTERIZED METHOD OF MATCHING TWO-DIMENSIONAL (2-D) PATTERNS



(57) Abstract

A computerized method (200) for use in data acquisition and manipulation of two-dimensional patterns in the fields of medicine, astronomy, chemistry, biology and biotechnology. The interactive computerized method (200) facilitates matching visual patterns of polypeptide spots in two-dimensional gel electrophoretograms solubilized into polypeptide constituents that are separated by electrophoresis. The computerized method (200) manipulates spot pixel coordinates using staged coordinate transformation techniques (251) on spot markers and unknown study spots to reduce gel preparation distortions and allows a user to produce matching results in an operation (252) that compares the tranformed spot data using either a single reference gel approach (255) or a multiple reference gels approach (254) for producing the matching results. The method also includes a spot matching verification step (252a) and a step (256) to extract potentially mismatched spots from reported matching results. The user can also resolve contradictions in resolve step (253) and perform spot matching analysis (270) using isoelectric focusing (PI), and molecular weight (MW) dimensional separation data.

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A COMPUTERIZED METHOD OF MATCHING TWO-DIMENSIONAL (2-D) PATTERNS

Field of the Invention

This invention relates to computerized methods for data acquisition and manipulation of two-dimensional patterns in the fields of medicine, astronomy, chemistry, biology and biotechnology. More particularly, the present invention relates to computerized methods for data manipulation of visual patterns of polypeptide spots in one-dimension (1-D) and two-dimensional (2-D) gel electrophoretograms, i.e. visual patterns of protein of cells (tissue, or body fluids), solubilized into polypeptide constituents that are separated by electrophoresis. Even more particularly, the present invention relates to interactive computerized methods of spot data acquisition and pixel coordinate manipulation involving coordinate transformation techniques and the use of isoelectric focusing (PI), and molecular weight (MW) dimensional separation properties during a spot matching task.

Description of the Prior Art:

In the biotechnology field, two-dimensional electrophoresis of polypeptides in polyacrylamide gel is a process known for separating the polypeptides, hereinafter also referred to as spots, in two dimensions, the first on the basis of charge by isoelectric focusing, the second on the basis of molecular weight by electrophoresis. The resulting two-dimensional gel electrophoretograms from this process contain spot patterns that are useful for analyzing cell types as well as the genetic metabolic activity of cells. Since the gels contain thousands of two-dimensional spot patterns having geometric characteristics that need to be visualized and manipulated for gel comparisons, the need for the computational and organizational power of a computer system is apparent. The visualization of the spots on the gel has been made possible by autoradiography or staining

techniques, silver-stained electrophoretograms producing adequate gel scanning data for analysis, although considered less accurate than autoradiograms. The efficiency of the results of a spot pattern matching analysis is measured in percentages of matched spots between gels and depends greatly on the accuracy and robustness of the underlying computer program that controls data acquisition, spot detection and spot pattern data comparison and matching tasks. Limitations in the accuracy of data acquisition from gel images are known to involve several factors including film noise, flaws in the gels, which may include localized stretching or actual physical breaks in the gels, streaking, which are protein complexes formed during gel preparations and other positional related distortions caused by added or subtracted charges that affect mobility of the protein in the gel or intensity related distortions caused by faintly staining proteins due to heterozygosity characteristics of a spot. Certainly, human intervention and introduction of artifactual informalities also factors into the equation of optimizing the matching task. Further, the equipment used to create gel images from which the positional and intensity data is obtained must also be scrutinized in optimizing the spot matching tasks.

The importance of pursuing and improving quantitative analysis of two-dimensional gels has been recognized in the biotechnology community and has produced the following prior art publications and patents that are of interest in considering the present invention.

For example, an article by P.F. Lemkin et al. entitled "GELLAB: A Computer System for 2D Gel Electrophoresis Analysis. II. Pairing Spots", Computers and Biomedical Research, Vol. 14, pp. 355-380 (1981).

An article by K.P. Vo et al, entitled "Computer Analysis of Two-Dimensional Gels", Analytical Biochemistry Vol. 112, pgs. 258-271 (1981).

An article by M.M. Skolnick et al., entitled "Computer Programs for Adapting Two-Dimensional Gels to the Study of Mutation", Clin. Chem. Vol. 28/4, pp. 969-978 (1982).

An article by M.J. Miller et al, entitled "Computer Analysis of Two-Dimensional Gels: Semi-Automatic Matching", Clin. Chem. Vol. 28/4, pgs. 867-875 (1982).

An article by M.J. Miller et al, entitled "Computer Analysis of Two-Dimensional Gels: Automatic Matching", Electrophoresis Vol. 5, pgs. 297-303 (1984).

An article by P. Vincens et al, entitled "HERMeS: A second generation approach to the automatic analysis of two-dimensional electrophoresis gels, Part III: Spot list matching", Electrophoresis Vol. 8, pgs. 100-107 (1987).

An article by A.D. Olson et al, entitled "Elsie 4: Quantitative Computer Analysis of Sets of Two-Dimensional Gel Electrophoretograms", Analytical Biochemistry Vol. 169, pgs. 49-70 (1988).

M.M. Skolnick et al., Chapter entitled "An Algorithm for Comparing Two-Dimensional Electrophoretic Gels, with Particular Reference to the Study of Mutations", in Advances in Human Genetics, Vol. 16, Chapter 2, pgs. 55-160, H. Harris & K. Hirschorn, Editors, (Plenum NY 1986).

M.M. Skolnick et al., in an article entitled "Computer Programs for Adapting Two-Dimensional Gels to the Study of Mutation", Clin. Chem. Vol. 28/4, pp. 969-978 (1982).

The prior art patents that relate to the field of the present invention concern computerized apparatus and method for spot quantitation, spot analysis, image data correspondence, spot detection, image analysis and comparison, all utilizing pixel x and y coordinate data as the primary physical characteristic of the spot or image. Included in the above teachings are U.S. Patent Nos. 4,638,456, 4,618,937, 4,592,089, 4,590,607, 4,389,670, 4,812,909, 4,811,218, 4,706,192, 4,741,043 and 4,825,388.

Although there have been many computerized advances in matching spots in 2-D gels, the prior art does not teach using staged coordinate transformations that firstly puts all of the designated marker spots that highlight a region or investigative pattern formed by spots in the gels being analyzed into a registered relationship with marker spots in a designated reference gel, and that secondly, applies the resulting marker spot registration relationship data to the coordinates of the remaining spots bounded by the marker spots, designated hereinafter as the unknown study spot members, to achieve x-y spot localization in the study gels having gel preparation distortional effects reduced to enable improved accuracy in spot location comparisons and improved matching efficiencies. Nor does the prior art teach the use of PI and MW gel preparation data in spot analysis of 2-D gels to improve spot matching interpretation between two or more 2-D gels.

Therefore, a need is believed to exist for an improved interactive computerized method of analyzing two-dimensional gel electrophoretograms that compensates for gel preparation distortional effects using staged coordinate transformation techniques prior to comparing and matching polypeptide spots contained in the 2-D gels.

Further, a need is seen to exist for an interactive computerized method for analyzing 2-D gels that uses staged coordinate transformation techniques and that also utilizes PI and MW preparation data that enables a user to combine the improved spot localization results associated with the transformation technique with the inherent accuracy associated with the PI and MW dimensional separation values that are at the heart of the electrophoresis process.

A need is seen to exist for an interactive computerized method for analyzing 2-D gels that utilizes the transformed spot data resulting from the staged coordinate transformation technique and that further performs matching

verification steps to assure that reported matching spots are indeed within target geometrical boundaries.

A further need is seen to exist for an interactive computerized method for analyzing 2-D gels whereby a user can extract potentially mismatched set of spots to improve the accuracy of reported matching results.

In the broader sense, a need is seen to exist for a computerized method for analyzing 2-D patterns in the fields of medicine, astronomy, chemistry, biology and biotechnology that uses staged coordinate transformation, matching verification and matching techniques that improve the accuracy and efficiency of a 2-D pattern matching task.

Summary of the Invention

Accordingly, the primary object of the present invention is to provide a computerized method of matching 2-D image data in the fields of medicine, astronomy, chemistry, biology and biotechnology having inherent distortional effects resulting from the initial image preparation process.

A specific object of the present invention is to provide an interactive computerized method of matching polypeptide spots in 2-D gels having inherent distortional effects resulting from the initial 2-D gel preparation process.

Another specific object of the present invention is to provide an interactive computerized method for resolving spot matching contradictions in spot clusters that inadvertently result during the comparing and matching steps.

Yet another specific object of the present invention is to provide an interactive computerized method for analyzing 2-D gels whereby a user can extract potentially mismatched set of spots to improve the accuracy of reported matching results.

A related object of the present invention is to provide PI and MW data for the 2-D gel spots being manipulated for use during an analysis of output data resulting from the comparing and matching subroutines to provide improved interpretation of the spot matching results.

According to one aspect of the invention, the foregoing objects are accomplished by a computerized method whereby each 2-D gel under investigation is scanned to generate an initial data file listing each spot's identification, the gel's name, each spot's original x-y coordinate values, each spot's integrated intensity, each spot's area, height and width. The user then designates one of the 2-D gels as a reference gel and the remaining gels as study gels and further designates in each gel, an investigative spot pattern of interest having a sufficient number of similarly positioned spots, generally prominent spots, referred to herein as reference marker spots in the reference gel and as study marker spots in the remaining study gels. The reference marker spots and the study marker spots form a boundary for the other spots within the spot patterns which are further designated as the unknown reference spots for the bounded spots in the reference gel and as unknown study spots for the bounded spots in the study gels. The user then further includes PI and MW for the designated reference and study marker spots in each of the gels for later utilization. At this point the user has effectively generated a modified initial data file for the scanned gels.

Using the modified initial data files, the user then executes several subroutines that: (1) adjust the original x-y coordinates of the spots in the investigative spot patterns in all gels by utilizing a two-stage coordinate transformation step and an interpolation step using the marker PI and MW data, (2) compare spot coordinates in a reference gel with spot coordinates in each study gel (referred to as a single reference match) to determine

potentially matching pairs of spots, or that compare spot coordinates in one gel with spot coordinates in the other gels, each time using one of the gels, including the previously designated reference gel, as a reference gel (referred to as multiple reference match), also to determine potentially matching pairs of spots, (3) perform a verification step that vectorially manipulates the potentially matching spot pair data to acertain whether a match spot pair or a non-matching spot pair exists, (4) resolve contradicting matching results, (5) compare matched spot data results against potentially mismatched spot data and potentially correctly matched spot data to improve accuracy, efficiency and confidence level of the matching results, and (6) that enables a user to manipulate the various data bases resulting from the operation of the subroutines for verifying the results as well as analyzing the data from different perspectives.

Therefore, to the accomplishments of the foregoing objects, the invention consists of the foregoing features hereinafter fully described and particularly pointed out in the claims, the accompanying drawings and the following disclosure describing in detail the invention, such drawings and disclosure illustrating but one of the various ways in which the invention may be practiced.

Brief Description of the Drawings:

Fig. 1 illustrates a typical hardware configuration for performing the interactive computerized method of matching protein spot patterns in 2-D gels in accordance with the present invention.

Fig. 2 illustrates a flow chart of the operations of a software program, that implements the present invention.

Fig. 2a illustrates a flow chart of the adjust operation portion of the present invention.

Figs. 2b, 2c and 2d illustrate a set of flow charts of the compare and match operation portion of the present

invention, that are used to determine potentially matching pairs of spots.

Fig. 2e illustrates a flow chart of the extract potential mismatch operation portion of the present invention, that compares the matching results with a file that contains matching results that are considered more likely to be correct.

Fig. 2f illustrates a flow chart of the resolve contraditions operation portion of the present invention that eliminates ambiguous matching results.

Fig. 3 illustrates a block diagram overview of a computer monitor screen illustrating a menu of the interactive computer software program, termed "MATCHWARE", that implements the present invention.

Fig. 4 is a detailed data flow chart of the operation of "MATCHWARE" software program that implements the present invention.

Fig. 5 illustrates a pair of gels in an overlay relationship to aid in understanding a vector analysis performed by the second transformation stage of present invention.

Fig. 5a illustrates a planer vector diagram based on the graphical gel overlay depicted in Fig. 5. illustrating a study spot's nearest marker spot and the next nearest marker spot.

Fig. 5b is a diagram illustrating an acceptable rectangular area for exact matching spots constructed by using the x and y components of vectors depicted in Fig. 5a shifted and having a common origin.

Description of the Preferred Embodiment

Referring first to Fig. 1 where a typical computer workstation 100 is illustrated as a means for performing the spot matching task of the present invention. System 100 includes a gel image processing system 110, commercially available under the trademark "VISAGE", a personal computer

120, such as a commercially available "IBM AT", or compatible, having a minimum system configuration, shown as unit 120b, of 640 kilo-bytes of random access memory, floppy disk storage capability, 10 mega-bytes of hard disk storage and enhanced graphics adapter card. Unit 120b is coupled to a display monitor 120a having color graphic display capability, a keyboard 120c, a mouse 120d for cursor manipulation. Output from the personal computer 120 can be by means of printer 130 for text data/graphical data and a plotter 140 for graphical display data. In the preferred embodiment printer 130 is a laser printer adapted for PostScript format, such as a Silentwriter LC 890, commercially available from NEC. Also, in the preferred embodiment, plotter 140 is a plotter compatible with HPGL graphic plotting format, commercially available as a FACIT 4550/4551.

Fig. 2 illustrates a flow chart summary of the steps involved in performing the 2-D gel matching task in accordance with the present invention. In the preferred embodiment, the steps are performed utilizing a software product 200 that will be commercially available under the trademark "MATCHWARE" from the University of Arizona in Tucson, Arizona forthwith filing of this patent application. Initially, a gel is scanned to produce gel spot data as indicated in steps 210 and 220. The manner of generating the initial spot data information is not the subject of the present invention, which generation of data includes the use of software programs that are known in the art and are thus not describe herein. The data generated includes the spot's identification, gel name, x-y coordinate values, integrated intensity, spot area, spot height and width. The state of the art being that the spot listing data available from these software programs cannot be used in its raw form to produce accurate and efficient spot comparison and spot matching task due to distortions present in the initial gel

preparation. Thus, in accordance with the present invention, further manipulation of the raw data is undertaken to compensate for the distortions.

The data available at computer 120 is typically a 1024 x 1024 pixel array of the gel images under investigation. Once the spot data is available at computer 120, and according to the data flow steps 230 and 240 shown in Fig. 2 and further referenced in Figs. 3 and 4, the user can manipulate the raw data, labeled .lst in Fig. 4 to designate which gel is to be the reference gel and which gel or gels are to be the study gel(s). The user can further manipulate the gel image to investigate a windowed spot pattern with dominant marker spots and all of the unknown numbered reference or study spots, depending upon which gel they are contained.

By example, Appendices C1, C2 and C3 provide data for three gels, labeled "a", "b" and "c", respectively which gels are used herein to aid in understanding the present invention. Appendix C provides a listing and description of data files generated by "MATCHWARE" during the spot matching task, Appendix C1-(1-6) contains the reference data for the gel labeled "a", including hardcopy of the gel's spot image and the windowed spot pattern of interest containing dominant marker spots labeled m in Appendix C1-1, and the corresponding spot data listing in Appendix C1-(2-6). The gel selected as the reference gel is generally determined by the operator as representing the best specimen from the group of gels, i.e. the one with the least visible distortions. Appendices C2-(1-7) and C3-(1-6) contain information about the two study gels labeled "b" and "c". Included in the Appendices C2 and C3 are hardcopy of the two study gel's spot images and the windowed spot patterns of interest containing dominant marker spots, also labeled m, in Appendices C2-1 and C3-1 and the corresponding spot data listing C2-(2-7) and C3-(2-6). Collectively, the data is

referred to as 210a for the reference gel and 210b and 210c for the two study gels in Fig. 4. The PI and MW data is also inputted for later use in the analysis as indicated in step 230 in Fig.4.

Once the gels under investigation are set up for analysis, step 250, as shown in Fig. 2, is executed to selectively perform various subroutines. Included in step 250 is a two-stage spot coordinate transformation step 251 (labeled adjust operation and shown in more detail flow chart in Fig. 2a and in appendices B(1-23) which comprise a source code listing of the adjust subroutine that performs the two-stage spot coordinate transformations), a comparison and match step 252 (shown in more detail in Figs. 2b, 2c and 2d) based on using multiple or single reference gels and supported by a resolve spot matching contradiction step 253 (shown in more detail in Fig. 2f) and an extract potential mismatched spots step 256 (shown in more detail in Fig. 2e). Appendices A(1-2) provide a brief description of the subroutine steps executed during the adjust operation illustrated in Fig. 2a. Similarly, Appendices A(3-5) provide a brief description of the subroutine steps executed during the compare and match operations illustrated in Figs. 2b, 2c and 2d. Appendix A6 provides a brief description of the solve cluster operation step executed during the resolve contradiction operation illustrated in Fig.2f. Appendix A7 provides a brief description of the solve cluster operation step executed during the extract potential mismatch operation illustrated in Fig.2e.

In the adjust operation 251, the two-stage coordinate transformation includes: (1) performing a first transformation step that transforms positional coordinates of the reference marker spot members and the unknown reference spot members in the reference gel, and each spot marker member in the study gel(s) set from the original scan coordinate system to a new reference coordinate system.

This first transformation step results in each member of the set of study marker spots being in a registered relationship with a corresponding spot marker member of the set of reference marker spots. It should be noted that the coordinates of the spot members in reference gel "a" remain the same after the first transformation. (2) performing a second transformation step that transforms positional coordinates of each of the unknown study spot members from the scan coordinate system to the reference coordinate system, the second transformation step comprises: (a) determining an effective range associated with each study marker spot, i.e. the distance associated with an influence which a dominant marker spot has over the surrounding spots which form a spot cluster. The effective range is calculated for each marker spot by locating the nearest marker neighbor to the marker spot and then assigning one-half of the distance between the marker and its nearest neighbor marker to be its effective range, (b) determining an attraction pairing relationship between a particular study marker spot member and a particular unknown study spot member, this attraction pairing relationship being determined by utilizing the effective range of the marker spots by a first rule for finding the nearest and second nearest markers to the unknown study spot, if this unknown study spot is within the effective range of the nearest marker, then the movement value of this unknown study spot into the new reference coordinate system is same as the movement value of the nearest marker spot. A second rule for determining the pairing relationship can be used if the current unknown spot is within the intersection of two times the effective range of the nearest and second nearest marker, then the movement value of this spot is same as the average movement value of the nearest and second nearest marker, otherwise the pairing relationship defaults to the first rule, (c) determining positional coordinates in the

reference coordinate system for each unknown study spot member by adjusting the original scan coordinates for each unknown study spot member by a shift amount, or movement values, equivalent to the first transformation shift amounts of the corresponding paired study marker spot member, and (d) repeating the pairing and new coordinate location determining steps for all unknown study spot members in a gel and for all gels being investigated. After the second transformation step, the PI and MW values of the unknown study spot members are determined using interpolation techniques based on PI and MW values previously assigned to the study marker spot members. Adjusted spot datafiles 251a (x.als), 251b (x.mks) and 251c (x.att) are produced as a result of the foregoing two-stage transformation and also include results of the PI and MW interpolation steps. Appendix C4-1) contains hardcopy printout of the windowed spot pattern and Appendices C4(2-4) contain corresponding spot datafiles 251a (a.als), 251b (a.mks) and 251c (a.att) for the reference gel that was manipulated by the 251 adjust operation, see Appendix C for file descriptors. Appendices C5-1 and C6-1 are also hardcopy printout of the windowed spot patterns for the two study gels "b" and "c", while Appendices C5(2-6) and C6(2-4) contain the corresponding spot datafiles 251a (b.als, c.als), 251b (b.mks, c.mks) and 251c (b.att, c.att), respectively, resulting from the two-stage spot coordinate transformation.

At this point in the analysis, all the necessary data to perform the comparing and matching tasks, denoted in Fig. 2 as operation 252 and depicted in the flow charts of Figs. 2b, 2c and 2d, is available. The comparing task primarily involves taking every identified unknown spot in each of the gels and analyzing the recorded data, using as required, the spot's old and new x-y coordinate values, integrated intensity, spot area, PI and MW data, spot height and width for comparing against similar data of the other unknown

spots and grouping the results as sets of potential matching spots. In the cases involving more than two study gels, the user has an option to either conduct a matching exercise based on using a single designated reference gel and comparing other study gels against and hence following the data flow using block 255 shown in Fig. 4 and in the flow chart of Fig. 2b, or conducting a matching exercise iteratively designating every gel as a reference gel, i.e. multiple reference gels and following the data flow using block 254, also as shown in Fig. 4 and in the flow chart of Fig. 2b.

Before a matched spots outcome is reported, i.e. based on exact matching coordinates, spot size or intensity, the present invention also performs a verification step 252a on the set of potentially matching spots, regardless of whether conducting a matching exercise according to operation step 254 or 255. The verification inquiry is part of the query depicted in the flow chart of Fig. 2d. Verification step 252a utilizes the potentially matching spot's nearest and next nearest marker spots, and their original positional data, to construct a pair of marker spot vectors for juxtaposition comparison with an unknown spot's vector formed by joining a first and second one of the potential matching unknown spots in two gels, also using the unknown spot's original positional data. Fig. 5 shows gel G1 and G2 in an overlay relationship where a first unknown spot G1S1, having nearest marker spot G1M1 and second nearest marker spot G1M2, supposedly matching second unknown spot G2S1, having nearest marker spot G2M1 and second nearest marker spot G2M2. The pair of marker spot vectors comprise a first vector V1 formed by graphically joining G1M1 to G2M1 and a second vector V2 formed by graphically joining G1M2 to G2M2, while the unknown spot's vector U1 is formed by graphically joining G1S1 to G2S1, see Fig. 5a. To maintain consistency in the vector's direction, one of the gels should be

designated as containing spots that form the tail of the vector and the other as containing spots that form the head of the vectors. The juxtaposition comparison requires shifting the three vectors such that their tails are on a common point to establish whether the head of the unknown spot's vector U1 falls within an acceptable rectangular area A1 formed by minimum and maximum x and y limits, see Fig. 5b for construction of the acceptable rectangular area A1, and vector U1's head falling within area A1 indicating that unknown spots G1S1 and G2S1 are a matching pair. The size of the acceptable rectangular area is based on x and y components of the head of vectors V1 and V2. The vertical boundaries are extended away from the actual x values for the V1 and V2 heads, while the upper y boundary is extended upward from the y value of the V2 vector and the lower boundary is extended downward from the y value of the V1 vector. The x and y amounts extended are user adjustable tolerance amounts, typically 0.5 milli-meters. If the head of vector U1 does not fall within the area A1, a no match situation exists for the particular pair of unknown spots, whose vector is being manipulated.

Assuming that a user wishes to manipulate the gel spot data based on multiple reference gel analysis, i.e. operation step 254, then the data flow depicted in Fig. 4 would result, see also Fig. 3 for subroutine options available. Following the data flow shown in Fig. 4 using operation step 254, the present invention addresses ambiguous situations in reported spot matching results (data file .mmh shown as 252b in Fig. 4) by processing the affected unknown spots through the resolve contradiction subroutine 253, as shown in Fig. 4 and also as shown in the flow chart in Fig. 2f. Appendices D1(1-3), D2, D3, D4(1-3),and D5(1-2) are gel group spot data manipulation results in accordance with the present invention wherein: Appendix D1 is a listing of datafile 252b (abc.mmh) based on multiple

reference gels, i.e. results based on each gel being used as a reference in the comparison task and includes matched and unmatched spots before resolving any contradictions contained in the data for the three gels under investigation. Appendix D2 is a listing of datafile 250c of a spot cluster exhibiting contradicting matching results which were extracted from datafile 252b and resolved by resolve contradiction subroutine 253, i.e. a spot(s) that is (are) found matching other spots that logically cannot be explained, for example one spot in one gel matched two spots and these two spots are in the same gel, (datafile 250c is an empty file upon resolving all contradictory clusters). Appendix D3 is a listing of datafile 250d of unmatched spots (termed "unique") as found in the three gels under investigation. Appendix D4(1-3) is a listing of datafile 250b of exact matched spots as determined by the present invention. Appendix D5(1-2) is a composite listing of datafile 250a of a pseudo gel, each member of the composite listing representing a matrix of matching spots having a plurality of rows, each row being identical to the corresponding member in the composite listing. In the 250a listing, negative record label represents matching spots, (two matching spots or three matching spots), while positive record label represents unmatched spots, as found in the three gels under investigation.

Referring now to Figs. 3 and 4, Appendix E1, is a listing of datafile 252c (abc.smh) similar to datafile 252b except generated using a designated single gel as a reference. Appendix E1 is generated by operation step 255 that is based on using a designated single gel as a reference gel and comparing it against each of the other study gels before generating the results. Datafile 252c has the characteristic that matched and unmatched spots are reported without any matching contradictions which normally results when the matching is based on a multiplicity of

reference gels. It has been observed that some of the matching spots results include mis-matched spot data and has led to reporting more matched spots in matching results listings, such as in Appendix E1, than actually exist. Faced with this potential error in matching results using a single gel as a reference gel, the user has the option of further manipulating the data using step 256 to extract potential mismatching spots to improve the accuracy of the match listings, see Fig. 4 and also the flow chart depicted in Fig. 2e. Step 256 allows the user to compare the datafile 252c against a composite datafile 250a, see Appendix D5(1-2), abc.cmp, (generated in background during operation of step 255 and contains the same data as if generated by operation 254, 253), which datafile abc.cmp contains matching results that are considered more likely to be correct. Comparison step 256 then generates potentially mis-matched spots datafile 256a, see Appendix E2, abc.pmm, and a potentially correctly matched spot datafile 256b, see Appendix E3, abc.pcm. In generating datafile 256a and 256b, it is noted that in comparing datafiles 252c against 250a that any potentially correct matching set of spots would be found in both datafile 250a and in 252c, while any potential mis-matched set of spots would be found only in datafile 252c, but not in 250a. Further, after step 256, it is noted that any potentially correct matching set of spots would be mostly found in datafile 256b and least in 256a, while any potential mis-matched set of spots would be found mostly in datafile 256a and least in 256b. Composite datafile 250a is given greater credibility because the matched set of spots found in datafile 250a are determined firstly as a matrix of matching spots using each gel as a reference gel and then repeated according to the number of gels under study. Having processed spot data through operation step 255, the user can then utilize datafile 256a containing the list of potentially mis-matched sets of spots as a means of

determining whether a particular set of matching spots being examined are part of the potentially mis-matched group of spot and thereby gain a higher confidence level about reported matching results, i.e. the matching results found in datafile 256b or 250b. The spot matching result listed in datafile 256b have an improved accuracy over those listed in datafile 252c in that the potential mis-matching spots have been sorted into datafile 256a.

Referring back to Fig. 2, the results from operation 250 may be reviewed in a variety of plotting options 260, see also Figs. 3 and 4, and may be repeatedly performed after analysis step 270 until a user has thoroughly understood the matching results, which step 270 takes advantage of having the PI and MW data to reinforce matching results based on comparisons in the new x and y coordinate system, and may be repeated using the data base information and may be based on inquiry 280, 281 that considers whether any further contradiction 253a exists, or whether new markers need to be considered, such as by looping back through marker designation step 230 and bypassing step 240.

Therefore, while the present invention has been shown and described herein in what is believed to be the most practical and preferred embodiments, it is recognized that departures can be made therefore within the scope of the invention, which is therefore not to be limited to the details disclosed therein but is to be accorded the full scope of the claims so as to embrace any and all equivalent methods.

ADJUST OPERATION

ReadMatchCfg	Get the gel names (i.e. file names) from match.cfg file. These files will be used to compare each other later. The first gel name will be the reference gel, the others are study gels.
ReadGetCfg	Get the PI and MW values of each marker. The PI and MW values stored in get.cfg are input by user via marker_entry program.
ReadListFiles	Get all the spot information of each gel.
AssignMarkers	Aligns all the markers of study gels to the markers of the reference gel. After alignment, all markers have the same X-Y value. The X-Y values of the reference gel are not changed. Calculates the effective range of each marker.
SetMarkersMove	Find out the movement value of each marker in the study gels. The movement value is got from the difference of old position and aligned position.
SetRefNewCoor	Set the new coordinate of the reference gel. (This new coordinate is same as old coordinate)
AdjustXY	Kicks out all the spots outside the window formed by markers. Call Adjust subroutine to adjust all the spots in each gel.
Adjust	Adjusts every unknown spot in the study gel by the following rules: 1. Find out the nearest and second nearest markers to this unknown spot. If this unknown spot is within the effective range of the nearest marker, then the movement value of this spot is same as the movement value of the nearest mark. 2. If rule 1 is not satisfied, use this rule. If the current unknown spot is within the intersection of two (2) times effective range of the nearest and

second nearest marker, then the movement value of this spot is same as the average movement value of the nearest and second nearest marker.

3. If rule 1 and rule 2 are not satisfied, then use rule 1 to get the movement value of the unknown spot.

AssignMkValues Assigns PI and MW values of the markers in each marker list.

CalMkBoundaryInfo Calculates the left, right, top, and bottom boundary delta x, y, PI, and MW for the using in GetPiMw subroutine.

GetPiMw Calculates the PI and MW values of each spot in each gel by using linear interpolation. The PI and MW values of each marker are input by user.

PrintAttMks Writes out the adjusted information and PI, MW value to the files. These files are ".als", ".att", and ".mks". The ".att" and ".mks" will be used in the comparison step.

NOTE: The algorithm to get the effective range of each marker:
Find out its nearest marker. Get half of the distance between this marker and its nearest marker to be its effective range.

COMPARISON OPERATION

OpenMatchCfg Gets the gel names (i.e. file names) from match.cfg file. These files will be used to compare each other later. The first gel name will be the reference gel, the others are study gels.

ReadMksAtt Gets the marker information of each gel in .mks and the spot information of each gel in .att.

Initialize Gives initial values to the internal parameters of the comparison routine.

Match2Gels* There is an iterative loop to call this routine to do the comparison in any pair of gels.

PrintOut In case that the match type is single reference match, writes the comparative result to the file (.smh), otherwise, writes the result to the file (.mmh). The ".smh" will be used in the extract mismatch; the ".mmh" will be used in the resolve cluster step.

NOTE: The asterisk (*) note means that the routine will be described detailedly later.

Match2Gels description

BuildRelOfMarkers Finds out the shift of markers between two gels.

InitMatch Gives initial value of tolerance, candidate range, minimum neighbor match number, and area threshold.

ClearMatch Finds out all the spot pair which are very close. All of these spot pairs are clear matched. Takes these spot pairs from the unmatched group.

Keep a fixed times loop to the following routines:

CalNewParameter Calculates the new parameters for criteria of comparison. If the spot pair satisfies these criteria, we say it is matched.

For each spot in first gel, do the following routines:

FindCandidate Finds out the match candidates (the spots in second gel which are fallen within the candidate range) for the current spot in the first gel.

Match2Spot* Compares pairs which are fallen within the candidate range.

ManyToOne Solves the status that two spots in the first gel matches with one spot in the second gel using some creteria. The scores of the previous and current matched pair depend on area ratio and shift length.

Match2Spot description

MatchPattern	Finds out the number of neighbors of the first gel which are matches with the neighbors of second gel. If the number is greater than or equal to the minimum neighbor match number, then call IsCorrectMove routine to double check matching, otherwise, call SecondChance routine to give another chance to this spot pair. The reason of the existing of IsCorrectMove and SecondChance is used to make up the defect of MatchPattern routine. In the case that the spot pair match is confirmed by IsCorrectMove, they are matched and taken from unmatched group, otherwise they are not matched. Same case will happen when the program calls SecondChance routine.
OneToMany	Solves the status that one spot in the first gel matches with two spots in the second gel using some creteria. The scores of the previous and current matched pair depend on area ratio and shift length.
IsCorrectMove	Finds out whether the spot shift is similar to the shift of it's near marker (includes shift length and shift angle).
SecondChance	Finds out whether the intensity and area ratio of the match pair spot is very similar to each other.

SOLVE_CLUSTER OPERATION

Opens the match.cfg file to get the file name which will be processed. Opens all the .mmh, .cmp, .exm, .cls, and .uni files.

1. **getpimw** Fetches PI and MW values from input file.

For each record in input file (.mmh), do the routines (2-5):

2. **get_record** Gets the record from input file (.mmh).

3. **get_gid** Finds out the gel index of a spot.

If the spot is a unique spot, then call put record to write out the spot to output, otherwise, do the routines: check pattern

4. **check_pattern** Does a pattern matching using the current record. If it is not matched in the cluster pattern, call cluster_insert routine to insert this new cluster into the cluster list. If it is matched, but it is not exact match, call update_pattern routine to update the pattern of the cluster, and call record_insert routine to insert a record into a cluster. If it is matched and it is exact match, call record_insert routine to insert a record into a cluster.

5. **cluster_insert** Inserts a new cluster into the cluster list.

6. **flush_pattern** Outputs all the outstanding patterns/records. If the record in the cluster is an exact match, call exact_flush routine to output the record, otherwise call resolve_cluster routine to resolve the cluster and output the record. In case that it is a single reference match, don't output .cls, .exm, snd .uni.

7. **sortcmp** Rearrange the order of .cmp file by increasing of PI value.

EXTRACT POTENTIAL MISMATCH

ReadCmp Gets the matched records from .cmp.

GetSmhRecord Reads one matched record from .smh each time. If there is no more record, the program is finished.

SameMatch Compares the record read in GetSmhRecord with record of .cmp by using the record number of the first gel (reference gel in single reference match) as key. If the comparison is same, call WritePcm, otherwise, call WriePmm. Jumps back to GetSmhRecord.

WritePcm Write the record read from .smh to .pcm (Potential Correct Match).

WritePmm Write the record read from .smh to .pmm (Potential Mis Match).

```
/*********************************************************
* adjust.h : header file of adjust.c                     *
* Author   : Wenjeng Ko                                  *
* Date     : November 1989                               *
*********************************************************/

#define DOS

#include <stdio.h>
#include <ctype.h>
#include <math.h>

#ifdef DOS
 #include <stdlib.h>
 #include <alloc.h>
#endif

#define NEWLINE         '\n'
#define EOS             '\0'
#define BLANK           ' '

#define bool            char

#define TRUE            1
#define FALSE           0

#define MAXLINE         128
#define MAX_GELS        35
#define MAX_MARKERS     50

#define MK_BASE         9000

#define X               0
#define Y               1
#define PI              0
#define MW              1

#define BELL            7

#define SQUARE(x)       ( (x) * (x) )


struct {      /* record #, pi, and mw of markers */
   int   rec;
   float pi, mw;
} mk_info[MAX_MARKERS];
```

APPENDIX B-1

```
typedef struct tspot {
    int  rec,      /* record number                          */
         x,        /* x-coord of the marker                  */
         y,        /* y-coord of the marker                  */
         newX,     /* new x-coord of the spot                */
         newY,     /* new y-coord of the spot                */
         pi,       /* pi value                               */
         mw,       /* mw value                               */
         h,        /* spot height                            */
         w;        /* spot width                             */
    char   name;   /* marker name                            */
    float  ii,     /* intergrate intensity of the spot       */
           area;   /* area                                   */
    struct tspot *next;     /* pointer to next spot          */
    struct tspot *prev;     /* pointer to previous spot      */
} SPOT;

typedef struct tmarker {
    int rec,               /* record number of markers */
        oldX, oldY,        /* old X and Y values       */
        newX, newY,        /* new X and Y values       */
        val,               /* the value of the marker  */
        name;              /* marker name              */
    float ii,              /* intensity                */
          area;            /* area                     */
    struct tmarker *next; /* pointer to next marker    */
} L_MARKER;

typedef struct {
    int rec,      /* record number of the spot          */
        oldX,     /* old x-coord of the spot            */
        oldY,     /* old y-coord of the spot            */
        newX,     /* new x-coord of the spot            */
        newY,     /* new y-coord of the spot            */
        effect_r,/* effect radius                       */
        idx,idy, /* individual dx & dy of each marker   */
        name;     /* name                               */
} MARKER;

typedef struct gel {
    char name[10];                    /* gel name          */
    int  number_of_spots;             /* number of spots   */
    SPOT *head;                       /* spot list header  */
    int  x_low,x_high,y_low,y_high;   /* selected window   */
    int  d_hpi,d_lpi,d_hmw,d_lmw;     /* delta of pi & mw  */
    int  d_hx,d_lx,d_hy,d_ly;         /* delta of x & y    */
    L_MARKER *Xmk_head;          /* X marker list header */
    L_MARKER *Ymk_head;          /* Y marker list header */
} GEL;
```

APPENDIX B-2

```
/*********************************************************
* adjust.c : adjust the coordinate of each spot in study  *
*            gel                                          *
* Author   : Wenjeng Ko                                   *
* Date     : November 1989                                *
*********************************************************/

#include "adjust.h"
#include "d:\turboc\csslib\twindow.h"

/*-------------------------------------------------------
|                  subroutine protocol                   |
-------------------------------------------------------*/
void    ReadGetCfg();
void    SetMarker();
void    MarkInsert();
void    AssignMarkers();
void    AdjustXY();
void    PrintAttMks();
MARKER  *GetNearestMark();
MARKER  *GetSecondNearestMark();
L_MARKER *MarkAlloc();
SPOT    *SpotAlloc();

/*-------------------------------------------------------
|                  global variables                      |
-------------------------------------------------------*/
WINDOW  *msgwnd;        /* message window pointer          */
FILE    *Fp_com;        /* file pointer for common use     */
int     Num_gels = 0;   /* number of gels                  */
GEL     Gels[MAX_GELS];/* gel information                  */
char    File_dir[40];   /* file directory                  */
int     Num_mk;         /* number of markers               */
MARKER  Markers[MAX_GELS][MAX_MARKERS]; /* marker info.    */
```

APPENDIX B-3

```
/* . . . . . */
main(argc, argv)
int argc;
char *argv[];
{
  int   i, j;
  char  cmd[80], cfg[55];
  char gelname[13], lstfile[55], mksfile[55], attfile[55];
  char file_dir[40], str[80];

  if (argc != 2) error("Usage: ", "adjust data_directory");

  strcpy(File_dir, argv[1]);

  Num_gels = ReadMatchCfg();

  ReadGetCfg();

  for (i = 0; i < Num_gels; i++)
    Gels[i].number_of_spots = ReadListFiles(i);

  /* Adjust x and y coordinates according to Ref. gel (gel[0]) */
  AssignMarkers(0);
  SetMarkersMove(0);
  SetRefNewCoor();

  for (i = 1; i < Num_gels; i++) {
    AssignMarkers(i);
    SetMarkersMove(i);
    AdjustXY(i);
  }

  for (i = 0; i < Num_gels; i++) {
    AssignMkValues(i);
    AssignNewXy(i);
  }

  /* Get the .mks and .att files in this step */
  for (i = 0; i < Num_gels; i++) {
    GetPiMw(i);
  }

  /* Print out the .att and .mks files */
  for (i = 0; i < Num_gels; i++) {
    PrintAttMks(i);
  }
}  /* main */
```

APPENDIX B-4

```
/* . . . . . */
AssignNewXy(idx)
int     idx;
{
  int         i, j;
  L_MARKER    *mp;

  mp = Gels[idx].Xmk_head;
  while (mp != NULL) {
    for (i = 0; i < Num_mk; i++) {
      if (mp->rec == Markers[idx][i].rec) {
          mp->newX = Markers[idx][i].newX;
          mp->newY = Markers[idx][i].newY;
        break;
      }
    }
    mp = mp->next;
  }  /* while */

  mp = Gels[idx].Xmk_head;
  j = 0;
  while (mp != NULL) {
    if (j == 0) {
      Gels[idx].d_hx = mp->newX - mp->next->newX;
      Gels[idx].d_hpi = mp->val - mp->next->val;
    }
    else if (j == Num_mk - 2) {
      Gels[idx].d_lx = mp->newX - mp->next->newX;
      Gels[idx].d_lpi = mp->val - mp->next->val;
    }
    mp = mp->next;
    j++;
  }  /* while */

  mp = Gels[idx].Ymk_head;
  while (mp != NULL) {
    for (i = 0; i < Num_mk; i++) {
      if (mp->rec == Markers[idx][i].rec) {
          mp->newX = Markers[idx][i].newX;
          mp->newY = Markers[idx][i].newY;
        break;
      }
    }
    mp = mp->next;
  }  /* while */

  mp = Gels[idx].Ymk_head;
  j = 0;
  while (mp != NULL) {
    if (j == 0) {
```

```
      Gels[idx].d_hy = mp->newY - mp->next->newY;
      Gels[idx].d_hmw = mp->next->val - mp->val;
    }
    else if (j == Num_mk - 2) {
      Gels[idx].d_ly = mp->newY - mp->next->newY;
      Gels[idx].d_lmw = mp->next->val - mp->val;
    }
    mp = mp->next;
    j++;
  }  /* while */
}  /* AssignNewXy */


/* . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . */
/*
  ReadMatchCfg --- Open match.cfg and get the Gel_list
                   (gel name table).
*/
static int ReadMatchCfg()
{
  char  line[MAXLINE+1], dm[15];
  int   i, num;

  /* Get the gel name from match.cfg file */
#ifdef UNIX
  sprintf(line, "%s//match.cfg", File_dir);
#endif
#ifdef DOS
  sprintf(line, "%s\\match.cfg", File_dir);
#endif
  if ((Fp_com = fopen(line, "r")) == NULL)
    error("Can't open file match.cfg ", "!");

  for ( i = 0; i < 4; i++)
    fgets(line, MAXLINE, Fp_com);
  num = 0;
  while (fscanf(Fp_com, "%s", Gels[num].name) != EOF) {
    if (strlen(Gels[num].name) > 6)
      error("Gel name is over 6 characters --> ",
            Gels[num].name);
    num++;
  }
  fclose(Fp_com);
  return num;
}  /* ReadMatchCfg */


/* . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . */
/*
  ReadGetCfg --- read marker infomation ( get.cfg )
```

```
*/
void ReadGetCfg()
{
  L_MARKER *mtp;
  char  str[MAXLINE];
  float pi, mw;
  int   i, j, chkcnt, rec, nummk;

#ifdef UNIX
  sprintf(str, "%s//get.cfg", File_dir);
#endif
#ifdef DOS
  sprintf(str, "%s\\get.cfg", File_dir);
#endif

  if ((freopen(str, "r", Fp_com)) == NULL)
    error("Can't open file ", str);

  fgets(str, MAXLINE, Fp_com);
  sscanf(str, "%d ", &nummk);

  for (i = 0; i < nummk; i++) {
    fgets(str, MAXLINE, Fp_com);
    sscanf(str, "%d %f %f ", &rec, &pi, &mw);
    mk_info[i].rec = rec;
    mk_info[i].pi  = pi;
    mk_info[i].mw  = mw;
  }
  fclose(Fp_com);

} /* ReadGetCfg */


/* . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . */
/*
  ReadListFiles --- read spot information from .lst file
*/
int ReadListFiles(idx)
int     idx;
{
  SPOT  *stemp;
  char  imagename[15], str[MAXLINE];
  int   i, rec, x, y, spotname, h, w, num;
  float ii, area;
  bool  is_marker;

#ifdef UNIX
  sprintf(str, "%s//%s.lst", File_dir, Gels[idx].name);
#endif
#ifdef DOS
```

```
  sprintf(str, "%s\\%s.lst", File_dir, Gels[idx].name);
#endif

  if ((freopen(str, "r", Fp_com)) == NULL)
    error("Can't open file ", str);

  for(i = 1; i <= 5; i++) fgets(str, MAXLINE-1, Fp_com);

  num = 0;
  while((fgets(str, MAXLINE, Fp_com)) != 0) {
    is_marker = FALSE;
    if (str[5] == BLANK)
      sscanf(str, "%d %s %d %d %f %f %d %d", &rec, imagename,
                    &x, &y, &ii, &area, &h, &w);
    else {
      is_marker = TRUE;
      sscanf(str, "%d %d %s %d %d %f %f %d %d", &rec, &spotname,

                  imagename, &x, &y, &ii, &area, &h, &w);
    } /* else */

    num++;
    if(is_marker == TRUE) rec = spotname + MK_BASE;
    stemp = SpotAlloc();
    stemp->rec  = rec;
    stemp->x    = x;
    stemp->y    = y;
    stemp->ii   = ii;
    stemp->area = area;
    stemp->h    = h;
    stemp->w    = w;
    SpotInsert(idx, stemp);
    if (is_marker == TRUE) SetMarker(idx, stemp);

  } /* while */

  fclose(Fp_com);

  return num;

} /* ReadListFiles */


/* . . . . . */
/*
  SpotInsert --- insert the node to list in decreasing order
        This is a double link list.
*/
static SpotInsert(which_gel, stemp)
int    which_gel;
```

```
SPOT    *stemp;
{
  SPOT *tp, *head;

  head = Gels[which_gel].head;

  if(head == NULL) {
    stemp->prev = NULL;
    Gels[which_gel].head = stemp;
    return;
  }

  tp = head;
  while (tp != NULL) {
    if (stemp->x <= tp->x) {
      if (tp->next == NULL) {     /* this is the last item */
        stemp->prev = tp;
        tp->next = stemp;
        break;
      }
      else {       /* this is not the last item */
        if (stemp->x >= tp->next->x) {
          stemp->prev = tp;
          stemp->next = tp->next;
          tp->next->prev = stemp;
          tp->next = stemp;
          break;
        }
        else {     /* go to next loop */
          tp = tp->next;
        }
      }
    }  /* if */
    else {   /* put in the first position */
      stemp->next = tp;
      stemp->prev = NULL;
      tp->prev = stemp;
      head = stemp;
      break;
    }
  }  /* while */
  Gels[which_gel].head = head;

}  /* SpotInsert */


/* . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . */
/*
  SetMarker --- link the marker to marker list
*/
```

```
void SetMarker(which_gel, stemp)
int      which_gel;
SPOT     *stemp;
{
   L_MARKER *mtemp;

   mtemp = MarkAlloc();
   mtemp->rec   = stemp->rec;
   mtemp->oldX = stemp->x;
   mtemp->oldY = stemp->y;
   mtemp->val   = stemp->pi;
   mtemp->name = stemp->name;
   MarkInsert(which_gel, mtemp, PI);

   mtemp = MarkAlloc();
   mtemp->rec   = stemp->rec;
   mtemp->oldX = stemp->x;
   mtemp->oldY = stemp->y;
   mtemp->val   = stemp->mw;
   mtemp->name = stemp->name;
   MarkInsert(which_gel, mtemp, MW);
} /* SetMarker */


/* . . . . . . . . . . . . . . . . . . . . . . . . . . . . . */
/*
  MarkInsert --- insert marker to marker list
*/
void MarkInsert(which_gel, mtemp, type)
L_MARKER *mtemp;
int      type, which_gel;
{
  L_MARKER *head, *tp, *prev;

  if (type == PI) head = Gels[which_gel].Xmk_head;
  else            head = Gels[which_gel].Ymk_head;

  tp = head;
  if(tp == NULL) head = mtemp;
  else {
    prev = head;

    while(tp != NULL) {
      if(type == PI && tp->oldX < mtemp->oldX) break;
      if(type == MW && tp->oldY < mtemp->oldY) break;
      prev = tp;
      tp = tp->next;
    } /* while */

    if(tp == prev) {
```

```
      mtemp->next = tp;
      head = mtemp;
    } /* if */
    else {
      mtemp->next = tp;
      prev->next = mtemp;
    } /* else */
  } /* else */

  if (type == PI) Gels[which_gel].Xmk_head = head;
  else            Gels[which_gel].Ymk_head = head;

} /* MarkInsert */
/* . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . */
void AssignMarkers(which_gel)
int     which_gel;
{
  L_MARKER   *m;
  int        xlow, xhigh, ylow, yhigh, mk_number;
  static int first = TRUE;

  xlow = ylow = 9999;
  xhigh = yhigh = -1;
  m = Gels[which_gel].Xmk_head;
  mk_number = 0;
  while (m != NULL) {
    if (m->oldX < xlow) xlow = m->oldX;
    if (m->oldX > xhigh) xhigh = m->oldX;
    if (m->oldY < ylow) ylow = m->oldY;
    if (m->oldY > yhigh) yhigh = m->oldY;

    Markers[which_gel][mk_number].rec  = m->rec;
    Markers[which_gel][mk_number].oldX = m->oldX;
    Markers[which_gel][mk_number].oldY = m->oldY;
    Markers[which_gel][mk_number].name = Num_mk;

    mk_number++;
    m = m->next;
  }
  if (mk_number < 3)
    error("Number of markers should be over 3", ".");
  if (mk_number > MAX_MARKERS)
    error("Number of markers should be less than 50", ".");
  if (first) {
    Num_mk = mk_number;
    first = FALSE;
  }
  else {
    if (mk_number != Num_mk)
      error(Gels[which_gel].name,
```

```
            " has different marker number.");
    }
    Gels[which_gel].x_low = xlow;
    Gels[which_gel].x_high = xhigh;
    Gels[which_gel].y_low = ylow;
    Gels[which_gel].y_high = yhigh;
}   /* AssignMarkers */
```

```
/* . . . . . . . . . . . . . . . . . . . . . . . . . . . . . */
/*
  SetMarkersMove : Compare markers in Gel i with Gel 0,
                   put the difference in idx and idy.
*/
SetMarkersMove(which_gel)
int     which_gel;
{
  MARKER      m;
  int         i, j;

  if (which_gel == 0) {       /* This is ref gel */
    for (i = 0; i < Num_mk; i++) {
      Markers[0][i].newX = Markers[0][i].oldX;
      Markers[0][i].newY = Markers[0][i].oldY;
      Markers[0][i].idx = Markers[0][i].idy = 0;
    }
    return;
  }

  for (i = 0; i < Num_mk; i++) {
    for (j = 0; j < Num_mk; j++) {
      if (Markers[which_gel][i].rec == Markers[0][j].rec)
        break;
    }
    Markers[which_gel][i].idx =
        Markers[0][j].oldX - Markers[which_gel][i].oldX;
    Markers[which_gel][i].idy =
        Markers[0][j].oldY - Markers[which_gel][i].oldY;
    Markers[which_gel][i].newX = Markers[0][j].oldX;
    Markers[which_gel][i].newY = Markers[0][j].oldY;
  }
}  /* SetMarkersMove */


/* . . . . . . . . . . . . . . . . . . . . . . . . . . . . . */
void AdjustXY(which_gel)
int     which_gel;
{
  SPOT   *sp;

  sp = Gels[which_gel].head;
  while (sp != NULL) {
  if (sp->x <= Gels[which_gel].x_high &&
      sp->x >= Gels[which_gel].x_low  &&
      sp->y <= Gels[which_gel].y_high &&
      sp->y >= Gels[which_gel].y_low )
    Adjust(which_gel, sp);
    sp = sp->next;
  }
```

```
}  /* AdjustXY */

/* . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . */
/*
  SetRefNewCoor --- Set the reference gel's new X, Y value.
*/
SetRefNewCoor()
{
  SPOT  *sp;

  sp = Gels[0].head;
  while (sp != NULL) {
    if (sp->x <= Gels[0].x_high &&
        sp->x >= Gels[0].x_low  &&
        sp->y <= Gels[0].y_high &&
        sp->y >= Gels[0].y_low ) {
      sp->newX = sp->x;
      sp->newY = sp->y;
    }
    sp = sp->next;
  }
}  /* SetRefNewCoor */


/* . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . */
/*
  Adjust --- Adjust the spots in the study gels to it's markers
*/
static Adjust(which_gel, sp)
int     which_gel;
SPOT    *sp;
{
  MARKER     *mark0, *mark1, *mark2;
  int        t1, t2, t3, t4, tx, ty;

  mark0 = GetNearestMark(which_gel, sp);
  mark1 = GetSecondNearestMark(which_gel, sp);

  t1 = mark0->oldX - sp->x;
  t2 = mark0->oldY - sp->y;
  t3 = mark1->oldX - sp->x;
  t4 = mark1->oldY - sp->y;
  if ( SQUARE(t1)+SQUARE(t2) <= SQUARE((long)mark0->effect_r) ) {
    tx = mark0->idx;
    ty = mark0->idy;
  }
  else if ( (SQUARE(t1) + SQUARE(t2) <= 4 *
             SQUARE((long)mark0->effect_r) ) &&
            (SQUARE(t3) + SQUARE(t4) <= 4 *
             SQUARE((long)mark1->effect_r) ) ) {
```

```
    tx = (mark0->idx + mark1->idx) / 2.0;
    ty = (mark0->idy + mark1->idy) / 2.0;
  }
  else {
    tx = mark0->idx;
    ty = mark0->idy;
  }

  sp->newX = sp->x + tx;
  sp->newY = sp->y + ty;

} /* Adjust */


/* . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . */
MARKER  *GetNearestMark(which_gel, node)
int     which_gel;
SPOT    *node;
{
  int   i;
  unsigned   long min = 9999999;
  long  dist;
  long  tp1, tp2;
  int   mark;

  for ( i = 0 ; i < Num_mk ; i++ ) {
    /* Since all Study-gels' marker.newX and marker.newY are
       equal to Ref-gel's, and we use newX, newY to find the
       nearest marker, therefore gel[Ref_gel]'s marker list
       can be use for every Study-gel's marker list
    */
    tp1 = node->x - Markers[which_gel][i].oldX;
    tp2 = node->y - Markers[which_gel][i].oldY;

    dist = SQUARE(tp1) + SQUARE(tp2);

    if ( dist < min ) {
      min = dist;
      mark = i;
    }
  }
  return( &Markers[which_gel][mark] );
}  /* GetNearestMark */


/* . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . */
MARKER  *GetSecondNearestMark(which_gel, node)
int     which_gel;
SPOT    *node;
{
```

```
    int   i;
    unsigned   long min1 = 9999999, min2 = 9999999;
    long  dist;
    long  tp1, tp2;
    int   mark1, mark2;

    for ( i = 0 ; i < Num_mk ; i++ ) {
      /* Since all Study-gels' marker.newX and marker.newY are
         equal to Ref-gel's, and we use newX, newY to find the
         nearest marker, therefore gel[Ref_gel]'s marker list
         can be use for every Study-gel's marker list
      */
      tp1 = node->x - Markers[which_gel][i].oldX;
      tp2 = node->y - Markers[which_gel][i].oldY;

      dist = SQUARE(tp1) + SQUARE(tp2);

      if ( dist < min1 ) {
        min2 = min1;
        mark2 = mark1;
        min1 = dist;
        mark1 = i;
      }
      else if (dist < min2) {
        min2 = dist;
        mark2 = i;
      }
    }
    return( &Markers[which_gel][mark2] );
}   /* GetSecondNearestMark */


/* . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . */
/*
  GetPiMw --- get PI & MW values for each spot
*/
GetPiMw(which_gel)
int      which_gel;
{
  SPOT   *sp;

  sp = Gels[which_gel].head;
  while( sp != NULL ) {
    if( sp->x >= Gels[which_gel].x_low &&
        sp->x <= Gels[which_gel].x_high &&
        sp->y >= Gels[which_gel].y_low &&
        sp->y <= Gels[which_gel].y_high ) {
      CalPi(which_gel, sp);
      CalMw(which_gel, sp);
    } /* if */
```

```
    else {
      sp->pi = -1000;
      sp->mw = -1000;
    }
    sp = sp->next;
  } /* while */
} /* GetPiMw */

/* . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . */
/*
  CalPi --- calculate the pi value of the spot
*/
CalPi(which_gel, sp)
int     which_gel;
SPOT    *sp;
{
  L_MARKER   *mp;
  int        i;
  long       t;

  mp = Gels[which_gel].Xmk_head;
  i = 0;
  while (mp != NULL) {
    if (sp->newX>mp->newX && i == 0) { /* over right margin */
      t = ((long) sp->newX - mp->newX) *
          Gels[which_gel].d_hpi /
          Gels[which_gel].d_hx - mp->val;
      sp->pi = (int) t;
      break;
    }
    else if (sp->newX == mp->newX) {
      sp->pi = mp->val;
      break;
    }
    else {
      if(mp->next != NULL) {
        if(sp->newX > mp->next->newX) {
          t = ((long) sp->newX - mp->next->newX) *
              (mp->val - mp->next->val) /
              (mp->newX - mp->next->newX);
          sp->pi = mp->next->val + (int) t;
          break;
        }
      }
      else {
        t = ((long) mp->newX - sp->newX) *
            Gels[which_gel].d_lpi /
            Gels[which_gel].d_lx;
        sp->pi = mp->val - (int) t;
        break;
```

```
        }
      }
      mp = mp->next;
      i++;
    }  /* while */
  } /* CalPi */
```

APPENDIX B-18

```
/* . . . . . . . . . . . . . . . . . . . . . . . . . . . */
/*
  CalMw --- calculate the mw value of the spot
*/
CalMw(which_gel, sp)
int      which_gel;
SPOT     *sp;
{
  L_MARKER    *mp;
  int         i;
  long        t;

  mp = Gels[which_gel].Ymk_head;
  i = 0;
  while (mp != NULL) {
   if (sp->newY>mp->newY && i == 0) {  /* over right margin */
       t = ((long) sp->newY - mp->newY) *
             Gels[which_gel].d_hmw /
             Gels[which_gel].d_hy;
       sp->mw = mp->val - (int) t;
       break;
   }
   else if (sp->newY == mp->newY) {
     sp->mw = mp->val;
     break;
   }
   else {
     if(mp->next != NULL) {
        if(sp->newY > mp->next->newY) {
          t = ((long) sp->newY - mp->next->newY) *
              (mp->val - mp->next->val) /
              (mp->newY - mp->next->newY);
          sp->mw = mp->next->val + (int) t;
          break;
        }
     }
      else {
        t = ((long) mp->newY - sp->newY) *
             Gels[which_gel].d_lmw /
             Gels[which_gel].d_ly;
        sp->mw = mp->val - (int) t;
        break;
      }
    }
    mp = mp->next;
    i++;
  }  /* while */
} /* CalMw */
```

```
/* . . . . . . . . . . . . . . . . . . . . . . . . . . . . */
/*
  AssignMkValue -- assign the value of marker to PI marker list
*/
static AssignMkValues(which_gel)
int     which_gel;
{
  L_MARKER   *mp;

  /* Assign pi values */
  mp = Gels[which_gel].Xmk_head;
  while (mp != NULL) {
    mp->val = (int) (mk_info[mp->rec-MK_BASE-1].pi * 100);
    mp = mp->next;
  }

  /* Assign mw values */
  mp = Gels[which_gel].Ymk_head;
  while (mp != NULL) {
    mp->val = (int) (mk_info[mp->rec-MK_BASE-1].mw * 100);
    mp = mp->next;
  }
} /* AssignMkValues */


/* . . . . . . . . . . . . . . . . . . . . . . . . . . . . */
/*
  MarkAlloc --- allocate the marker node in memory
*/
static L_MARKER *MarkAlloc()
{
  L_MARKER *mtemp;

  if( (mtemp = (L_MARKER *)malloc(sizeof(L_MARKER))) == NULL )
    error("Out of memory","!");

  mtemp->val = -1000;
  mtemp->next = NULL;
  return(mtemp);
} /* MarkAlloc */


/* . . . . . . . . . . . . . . . . . . . . . . . . . . . . */
/*
  SpotAlloc --- allocate the spot node in memory
*/
SPOT *SpotAlloc()
{
  SPOT *stemp;
```

```
  if( (stemp = (SPOT *)malloc(sizeof(SPOT))) == NULL )
    error("Out of memory","!");
  stemp->pi   = -1000;
  stemp->mw   = -1000;
  stemp->newX = -1;
  stemp->newY = -1;
  stemp->next = NULL;
  stemp->prev = NULL;

  return(stemp);
} /* SpotAlloc */


/* . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . */
void PrintAttMks(which_gel)
int     which_gel;
{
  SPOT  *stemp, *stp;
  L_MARKER   *mtemp, *mtp, *tmp[MAX_MARKERS];
  int   i;
  char  str[55];

  /* Print out the .att files */
#ifdef UNIX
  sprintf(str, "%s//%s.att", File_dir, Gels[which_gel].name);
#endif
#ifdef DOS
  sprintf(str, "%s\\%s.att", File_dir, Gels[which_gel].name);
#endif

  if ((freopen(str, "w", Fp_com)) == NULL)
    error("Can't open file ", str);

  fprintf(Fp_com, "Filename: %s.att\n\n", Gels[which_gel].name);
  fprintf(Fp_com,
    "Rec#  X___ Y___ NewX NewY PI____ MW____ II_____ Area___ Ht__
Wd__\n");

  stemp = Gels[which_gel].head;
  while( stemp != NULL ) {
    if( stemp->pi != -1000 && stemp->mw != -1000 ) {
      fprintf(Fp_com,
        "%4d  %4d %4d %4d %4d %6.2f %6.2f %7.3f %7.3f %4d %4d\n",
            stemp->rec, stemp->x, stemp->y,
            stemp->newX, stemp->newY,
            stemp->pi/100.0, stemp->mw/100.0, stemp->ii,
            stemp->area, stemp->h, stemp->w);
    }
    stp = stemp;
    stemp = stemp->next;
```

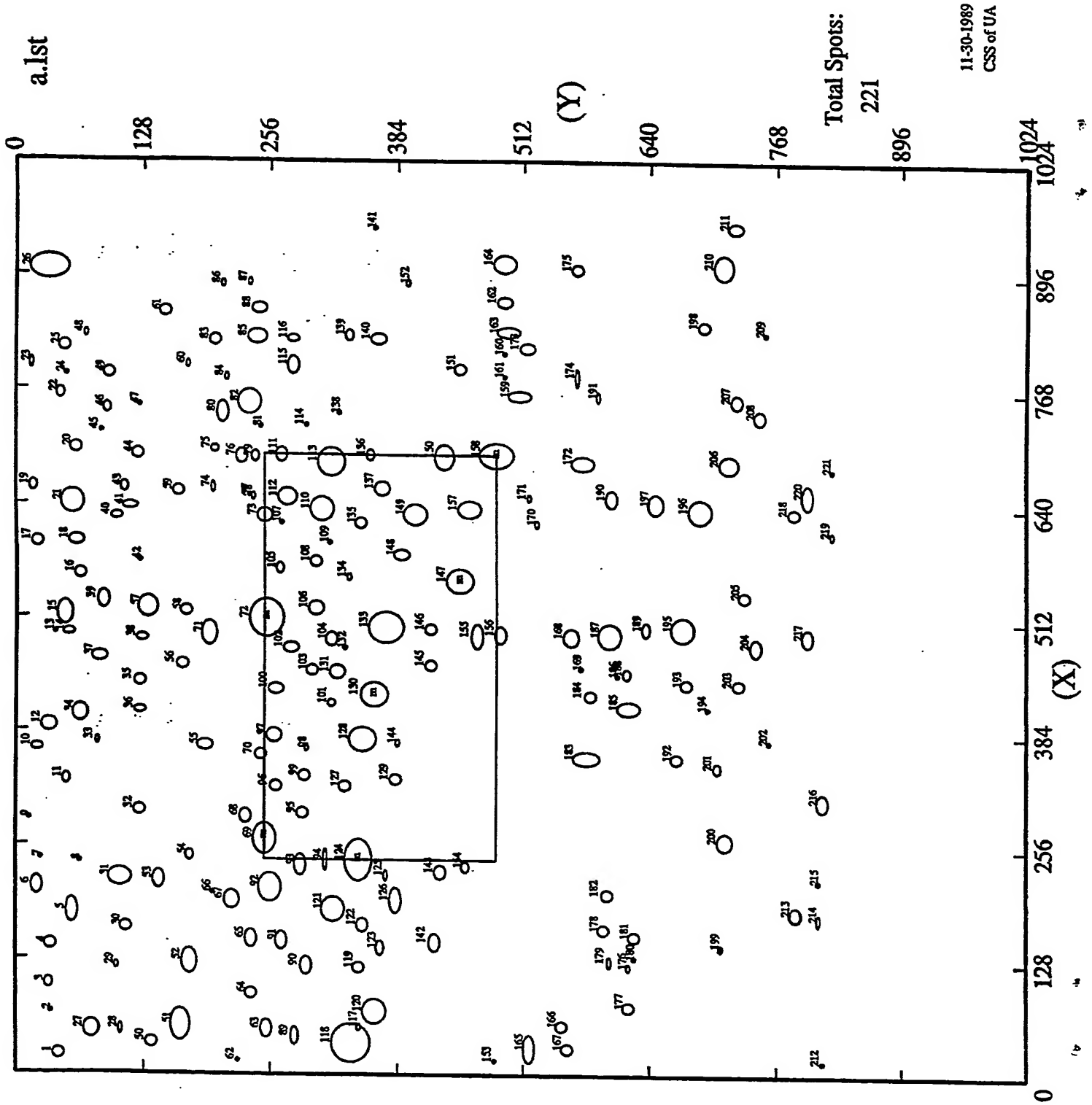
```
  } /* while */
  fclose(Fp_com);


  /* Print out the .als (modified .lst) files.  The spots outside
   window will be ignored.
  */
#ifdef UNIX
  sprintf(str, "%s//%s.als", File_dir, Gels[which_gel].name);
#endif
#ifdef DOS
  sprintf(str, "%s\\%s.als", File_dir, Gels[which_gel].name);
#endif

  if ((freopen(str, "w", Fp_com)) == NULL)
    error("Can't open file ", str);

  fprintf(Fp_com, "Filename: %s.als\n", Gels[which_gel].name);
  fprintf(Fp_com, "Window = X : %4d ~ %4d\n",
        Gels[which_gel].x_low, Gels[which_gel].x_high);
  fprintf(Fp_com, "          Y : %4d ~ %4d\n\n",
        Gels[which_gel].y_low, Gels[which_gel].y_high);
  fprintf(Fp_com,
    "Rec# Spotname__ Image_____ NewX NewY II_____ Area___ Ht__
Wd__\n");

  stemp = Gels[which_gel].head;
  while( stemp != NULL ) {
    if( stemp->pi != -1000 && stemp->mw != -1000 ) {
      if (stemp->rec >= MK_BASE)
        fprintf(Fp_com,"%4d %-10d %-10s %4d %4d %7.3f %7.3f %4d
%4d\n",
              stemp->rec, stemp->rec-MK_BASE,
              Gels[which_gel].name,
              stemp->newX, stemp->newY, stemp->ii,
              stemp->area, stemp->h, stemp->w);
      else
        fprintf(Fp_com,"%4d %-10s %-10s %4d %4d %7.3f %7.3f %4d
%4d\n",
              stemp->rec, " ", Gels[which_gel].name,
              stemp->newX, stemp->newY, stemp->ii,
              stemp->area, stemp->h, stemp->w);
    }
    stp = stemp;
    stemp = stemp->next;
    free(stp);
  } /* while */
  fclose(Fp_com);

  /* Print out the .mks files */
```

```
#ifdef UNIX
  sprintf(str, "%s//%s.mks", File_dir, Gels[which_gel].name);
#endif
#ifdef DOS
  sprintf(str, "%s\\%s.mks", File_dir, Gels[which_gel].name);
#endif

  if ((freopen(str, "w", Fp_com)) == NULL)
    error("Can't open file ", str);

  fprintf(Fp_com, "%s.mks\n", Gels[which_gel].name);
  fprintf(Fp_com, "Window = X : %4d ~ %4d\n",
    Gels[which_gel].x_low, Gels[which_gel].x_high);
  fprintf(Fp_com, "          Y : %4d ~ %4d\n",
    Gels[which_gel].y_low, Gels[which_gel].y_high);

  /* sort the markers by record number */
  mtemp = Gels[which_gel].Xmk_head;
  for( i = 0; i < Num_mk; i++ ) {
    tmp[mtemp->rec - MK_BASE] = mtemp;
    mtemp = mtemp->next;
  } /* for */

  fprintf(Fp_com,
    "\n------------ %2d Markers ------------\n", Num_mk);
  fprintf(Fp_com, "Marker_name  X___  Y___\n");
  for( i = 1; i <= Num_mk; i++ ) {
    fprintf(Fp_com, "    %4d       %4d  %4d\n",
        tmp[i]->rec, tmp[i]->oldX, tmp[i]->oldY);
  } /* for */
  fclose(Fp_com);
}  /* PrintAttMks */


/* . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . */
/*
  error --- give the error message
*/
error(s1, s2)
char *s1, *s2;
{
  error_message(s1, s2, 0, OK);
  exit(1);
} /* error */

/*==================  end of adjust.c  ==================*/
```

Documentation Conventions

.lst = raw data file (X-Y coordinate)
.als = adjusted data file (X-Y coordinate) after run "match"
.att = adjusted data file (PI-MW coordinate) after run "match"
.mks = information about the markers
.mmh = multiple reference matched image file
.smh = single reference matched image file
.cmp = composite match image file
.pno = reference file for reading .cmp map
.exm = exact match spots file
.cls = cluster spots file
.uni = unique spots file
.pmm = potential mismatched spots
.pcm = potential correct matched spots
.lmt = metafile for drawing spot list map (X-Y coordinate)
.amt = metafile for drawing spot list map (PI-MW coordinate)
.cmt = metafile for drawing compositive map
.mmt = metafile for drawing the moving vector in any two matched gels
xdrawout.plt = output file for HPGL and PostScript of printer or plotter
get.cfg = configuration file of get pots
match.cfg = configuration file of match
draw.cfg = configuration file of comparison of .att and .cmp

APPENDIX C



APPENDIX C1-1

215		a	220	811	0.024	0.08	2	6
125		a	222	372	0.204	0.48	8	14
143		a	226	427	0.220	1.59	14	20
154		a	232	453	0.077	0.77	10	16
93		a	234	288	1.257	2.09	16	26
8		a	236	63	0.005	0.08	2	6
7		a	240	25	0.013	0.11	2	8
94		a	240	312	0.531	1.19	8	26
124	6	a	240	346	7.771	7.79	32	52
54		a	244	175	0.075	0.64	10	16
69	5	a	264	250	3.127	4.59	26	38
200		a	264	715	0.298	1.91	18	22
9		a	286	13	0.019	0.11	2	8
68		a	290	230	0.636	1.59	16	20
95		a	292	290	0.296	1.54	16	18
32		a	296	124	0.121	1.17	16	16
216		a	310	814	0.665	1.59	12	24
96		a	322	261	0.150	0.98	16	14
127		a	324	332	0.191	1.30	12	18
11		a	328	49	0.060	0.74	10	14
129		a	332	382	0.074	0.93	12	14
99		a	334	291	0.162	1.11	14	14
201		a	346	707	0.071	0.82	10	14
183		a	356	576	0.547	2.41	30	20
192		a	356	667	0.095	0.95	14	16
70		a	358	246	0.250	1.11	16	14
10		a	364	20	0.301	0.74	14	12
98		a	366	294	0.026	0.27	4	10
55		a	368	190	0.339	1.72	18	18
33		a	372	80	0.054	0.50	8	10
144		a	372	385	0.051	0.37	6	12
202		a	374	759	0.004	0.11	2	8
128		a	376	349	3.781	5.19	30	32
97		a	380	259	0.702	1.96	20	20
12		a	388	33	1.646	2.04	20	20
34		a	402	64	1.203	2.01	18	22
36		a	408	124	0.096	1.14	16	12
185		a	414	618	0.532	2.36	24	20
194		a	414	697	0.007	0.11	2	8
101		a	416	317	0.131	0.61	10	12
130	4	a	426	360	4.162	3.90	32	28
184		a	426	578	0.197	1.30	16	16
100		a	432	261	0.884	1.91	18	18
35		a	440	123	0.268	1.30	16	16
193		a	440	677	0.181	1.33	14	18
203		a	440	728	0.125	1.11	14	16
186		a	450	607	0.006	0.08	2	6
131		a	452	324	1.888	2.17	20	20
188		a	452	615	0.086	0.72	10	14
103		a	454	298	0.437	0.98	12	16
169		a	458	569	0.005	0.08	2	6
56		a	460	166	0.213	1.35	16	14
145		a	460	417	0.140	1.14	14	16
37		a	468	83	1.004	1.86	18	18

Print file name: a.lst, Time: 15:15 Date: 12/1/1989 Page:

Spotlist for 'a'. Image size 1024 x 1024. 221 spots.

Rec	Spotname	Image	X	Y	II	Area	Ht	Wd
62		a	16	222	0.044	0.16	4	6
153		a	16	482	0.060	0.32	8	6
212		a	16	814	0.052	0.16	4	6
1		a	22	42	0.391	1.40	14	18
165		a	30	517	0.740	2.89	14	36
167		a	30	555	0.158	0.93	12	18
50		a	36	135	0.236	1.19	14	18
118		a	36	337	10.508	6.84	42	46
89		a	44	280	0.210	1.14	10	24
27		a	50	74	1.438	2.23	18	24
28		a	50	104	0.064	0.69	8	16
63		a	52	252	0.921	1.91	16	22
117		a	54	346	0.214	0.24	4	10
51		a	56	165	3.456	4.13	22	38
166		a	56	550	0.128	0.95	12	16
2		a	70	35	0.006	0.08	2	6
120		a	72	360	2.635	2.70	24	28
177		a	78	618	0.162	1.27	14	18
64		a	92	238	0.100	1.01	12	16
3		a	102	32	0.102	0.64	10	14
29		a	120	100	0.026	0.61	8	12
119		a	122	346	0.277	1.33	14	18
90		a	124	292	0.523	1.75	16	22
176		a	124	618	0.026	0.27	4	10
52		a	126	174	1.358	2.62	18	28
179		a	130	598	0.063	0.69	8	14
180		a	132	625	0.007	0.08	2	6
123		a	142	367	0.199	1.09	10	20
4		a	144	34	0.146	0.66	12	14
199		a	146	711	0.004	0.08	2	6
142		a	148	421	0.468	1.72	16	24
91		a	150	268	0.392	1.46	12	22
65		a	152	236	0.704	1.86	16	22
181		a	156	624	0.123	0.95	12	16
30		a	164	110	0.076	0.74	12	14
178		a	164	592	0.096	0.95	12	14
122		a	168	349	0.412	1.48	14	20
214		a	178	810	0.140	0.32	4	14
5		a	180	55	0.823	2.46	14	34
213		a	184	786	0.226	1.33	12	20
121		a	186	321	2.968	4.16	26	34
67		a	194	217	0.764	1.99	18	22
126		a	194	383	0.795	2.07	14	30
66		a	202	198	0.023	0.16	4	6
182		a	204	596	0.216	1.46	16	18
6		a	208	20	0.565	1.35	12	24
92		a	208	256	3.188	4.66	26	36
53		a	216	142	0.179	1.46	12	22
31		a	218	104	0.555	2.65	24	22

102		a	478	277	1.250	1.54	20	16
132		a	480	333	0.039	0.08	2	6
204		a	484	746	0.237	1.54	14	22
38		a	490	126	0.159	0.80	14	10
104		a	490	319	1.404	1.38	14	20
155		a	492	464	0.379	1.91	16	32
168		a	492	559	0.681	2.54	20	24
13		a	494	38	0.043	0.16	4	6
187		a	494	598	0.907	2.36	24	28
14		a	496	52	0.279	0.82	12	12
71		a	496	194	0.813	1.83	18	30
156		a	496	487	0.190	1.35	12	22
217		a	496	799	0.624	1.80	14	24
146		a	500	417	0.203	1.30	14	18
195		a	502	672	2.796	4.29	24	34
133		a	504	372	3.676	5.80	36	38
189		a	504	635	0.210	1.14	10	20
72	3	a	512	252	8.928	6.71	38	46
15		a	518	48	1.571	2.46	20	28
58		a	520	171	0.472	1.40	14	18
57		a	524	132	0.875	2.84	22	26
106		a	524	302	1.773	2.33	20	20
39		a	532	86	0.669	1.88	16	22
205		a	540	735	0.168	1.25	14	18
147	2	a	556	447	4.757	5.12	32	32
134		a	560	336	0.055	0.48	8	12
16		a	562	62	0.234	1.17	14	16
105		a	570	265	0.052	0.72	10	14
42		a	576	125	0.003	0.08	2	6
108		a	576	302	0.111	1.09	12	18
148		a	586	389	0.264	1.54	18	16
17		a	596	21	0.223	1.06	14	14
18		a	600	59	0.283	1.46	18	14
109		a	600	316	0.022	0.19	4	8
219		a	610	823	0.228	0.32	6	12
107		a	620	268	0.049	0.19	4	8
135		a	620	348	0.281	1.14	14	16
170		a	620	524	0.028	0.19	4	10
40		a	626	100	0.103	0.66	12	12
73		a	628	250	1.006	1.80	20	20
149		a	630	402	1.845	2.86	24	26
218		a	634	785	0.433	1.09	14	14
110		a	636	308	2.391	3.34	24	30
157		a	636	457	1.162	2.20	28	24
196		a	636	690	2.274	3.79	26	30
41		a	638	115	0.233	0.87	18	10
21		a	642	56	1.827	3.37	26	32
197		a	644	646	1.267	2.09	20	26
78		a	650	239	0.037	0.13	2	10
112		a	650	274	1.391	1.67	22	22
171		a	650	517	0.064	0.34	6	10
190		a	650	601	0.569	1.40	16	22
77		a	652	235	0.021	0.08	2	6
220		a	654	799	0.975	1.64	12	30

59		a	656	162	0.409	1.54	16	18
43		a	658	109	0.200	0.90	10	16
74		a	658	198	0.110	0.58	8	14
137		a	658	369	0.859	1.99	20	20
19		a	660	16	0.423	0.90	10	16
221		a	684	823	0.054	0.11	2	8
172		a	688	571	0.870	2.57	24	20
206		a	688	719	0.933	2.78	22	24
113		a	690	319	3.868	5.06	32	36
76		a	694	227	0.741	1.30	14	20
79		a	694	241	0.508	0.93	10	18
150		a	694	430	1.023	2.62	22	30
44		a	696	122	0.319	1.01	12	16
136		a	696	357	0.300	1.03	10	18
158	1	a	696	484	3.652	5.14	36	28
111		a	698	267	0.641	1.30	12	20
20		a	702	60	0.414	1.03	12	18
75		a	702	199	0.150	0.61	10	12
45		a	722	84	0.016	0.19	4	8
81		a	728	247	0.014	0.08	2	6
114		a	730	292	0.026	0.16	4	8
208		a	742	751	0.254	1.62	14	20
80		a	744	207	0.942	2.23	16	26
138		a	744	327	0.006	0.08	2	6
46		a	748	91	0.055	0.77	10	14
47		a	752	124	0.010	0.19	4	8
82		a	756	235	2.450	3.37	26	28
207		a	760	727	0.277	1.33	16	20
22		a	762	45	0.081	0.77	10	14
159		a	762	508	0.507	2.17	24	18
191		a	762	588	0.068	0.72	8	16
84		a	782	211	0.032	0.29	6	10
174		a	784	566	0.068	0.64	8	22
24		a	786	49	0.004	0.08	2	6
161		a	786	492	0.021	0.16	4	6
49		a	788	94	0.157	1.48	16	18
151		a	794	446	0.044	0.82	12	14
23		a	796	15	0.042	0.45	6	14
60		a	796	172	0.024	0.48	8	12
115		a	796	279	0.267	1.62	14	22
160		a	810	491	0.011	0.08	2	6
25		a	816	48	0.148	0.98	12	16
173		a	816	515	0.401	1.59	18	18
83		a	824	199	0.408	1.43	16	16
116		a	826	279	0.108	0.82	14	10
140		a	826	365	0.408	1.78	18	18
85		a	828	242	1.843	2.39	22	20
48		a	830	69	0.042	0.40	6	12
139		a	830	335	0.112	0.80	10	14
163		a	834	495	0.470	1.75	24	16
209		a	834	756	0.005	0.16	4	8
198		a	842	693	0.064	0.82	14	14
61		a	856	150	0.270	1.14	16	14
88		a	858	244	0.772	1.46	20	14

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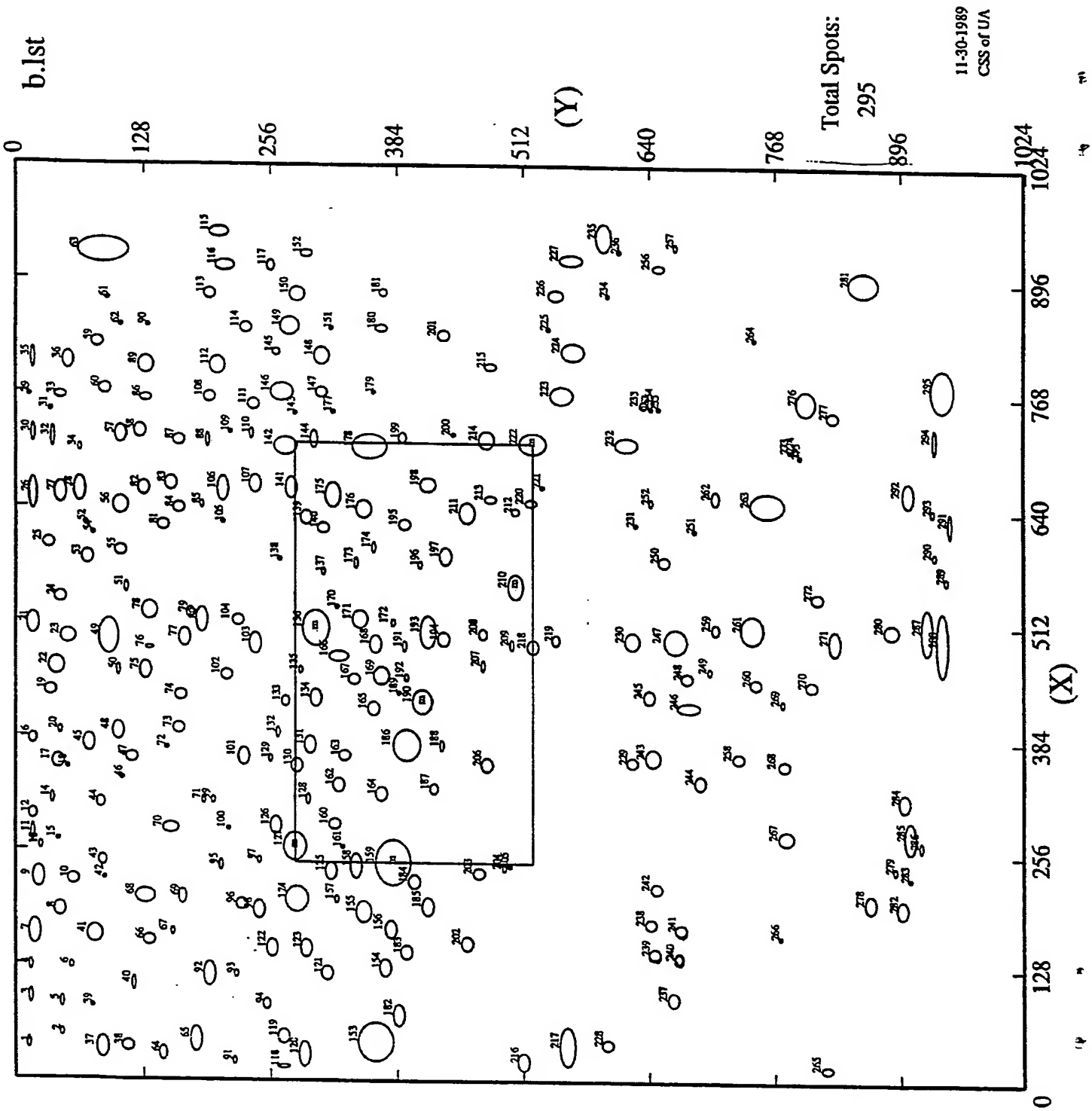
162	a	866	491	0.215	1.54	18	14
86	a	886	206	0.098	0.24	4	12
87	a	888	235	0.124	0.32	6	10
152	a	888	395	0.024	0.13	2	10
26	a	904	33	7.066	7.39	42	34
175	a	906	566	0.526	1.38	16	18
210	a	908	713	2.324	3.31	22	30
164	a	910	491	2.067	3.13	26	24
141	a	948	361	0.018	0.08	2	6
211	a	952	725	1.191	1.70	18	18



APPENDIX C2-1

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Spotlist for 'b'. Image size 1024 x 1024. 295 spots.

Rec	Spotname	Image	X	Y	II	Area	Ht	Wd
118		b	16	270	0.071	0.48	12	6
265		b	18	821	0.266	0.98	16	10
91		b	22	219	0.059	0.32	6	12
216		b	22	512	0.370	1.33	14	22
64		b	30	147	0.174	1.06	10	20
120		b	30	291	0.339	1.01	14	34
37		b	36	86	1.822	2.09	16	26
38		b	38	113	0.258	1.11	12	18
1		b	40	14	0.129	0.32	4	16
217		b	40	555	2.110	3.66	18	46
228		b	42	597	0.132	1.19	12	18
153		b	44	363	9.850	8.32	40	46
65		b	48	179	1.544	2.44	14	34
119		b	50	270	0.860	1.62	16	20
2		b	52	46	0.019	0.21	4	10
182		b	74	386	1.421	1.72	16	26
39		b	82	78	0.007	0.16	4	8
5		b	86	46	0.083	0.66	8	16
94		b	86	253	0.094	0.87	10	14
3		b	92	15	0.438	0.74	6	20
237		b	94	664	0.239	1.43	14	20
40		b	108	118	0.037	0.56	8	20
92		b	118	194	1.748	2.52	16	32
93		b	118	221	0.005	0.13	2	10
121		b	122	315	0.345	1.40	14	20
4		b	126	15	0.240	0.56	6	16
6		b	126	55	0.034	0.29	6	10
154		b	126	372	0.339	1.38	12	22
240		b	140	670	0.063	0.77	10	14
183		b	144	394	0.316	1.11	12	20
239		b	144	645	0.082	0.93	12	14
122		b	148	258	1.080	1.91	16	22
123		b	148	292	0.418	1.54	12	24
202		b	154	454	0.712	1.59	16	20
66		b	156	133	0.112	1.03	12	16
41		b	162	79	0.669	1.72	18	22
7		b	164	19	1.405	2.12	14	30
266		b	164	773	0.002	0.08	2	6
67		b	166	156	0.034	0.37	8	10
156		b	170	378	0.714	1.72	16	22
241		b	172	673	0.189	1.27	14	16
238		b	178	641	0.128	1.11	14	16
155		b	188	352	2.186	2.65	20	26
8		b	190	45	0.600	1.33	14	20
98		b	192	243	0.645	1.70	14	22
185		b	196	415	0.704	1.62	14	24
96		b	198	227	0.469	1.43	14	18
282		b	198	898	0.883	1.27	12	22
278		b	202	865	0.194	1.46	14	22

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124		b	204	284	2.900	3.47	24	30
157		b	204	323	0.076	0.37	6	12
68		b	206	130	0.842	2.23	22	20
69		b	206	167	0.178	1.06	10	20
242		b	216	647	0.168	1.19	14	16
10		b	222	58	0.199	0.93	12	18
184		b	222	402	0.949	1.33	16	20
9		b	224	22	2.169	2.44	16	26
42		b	224	89	0.008	0.08	2	6
283		b	230	905	0.039	0.08	2	6
203		b	232	466	0.172	1.09	14	16
125		b	234	318	1.405	2.04	16	24
204		b	238	491	0.024	0.37	6	10
95		b	240	205	0.043	0.40	6	14
158		b	240	344	1.004	1.83	12	30
205		b	242	497	0.003	0.08	2	6
279		b	242	890	0.045	0.27	4	10
43		b	244	87	0.125	0.90	10	16
159	6	b	244	381	11.183	9.49	40	54
97		b	246	244	0.051	0.42	8	10
13		b	260	24	0.243	0.56	8	12
127	5	b	262	281	4.348	4.35	26	36
161		b	262	330	0.035	0.19	4	8
15		b	268	41	0.061	0.29	6	8
286		b	268	917	0.454	0.50	6	18
11		b	274	16	0.836	0.93	8	22
267		b	276	779	0.321	1.86	18	20
285		b	278	907	1.623	1.33	12	40
70		b	282	155	0.250	1.43	18	18
100		b	282	213	0.012	0.24	6	8
126		b	284	261	0.806	1.56	14	22
160		b	288	322	0.489	1.56	16	18
12		b	296	17	0.317	0.82	10	14
44		b	310	85	0.169	0.98	10	18
14		b	312	36	0.144	0.72	8	18
71		b	312	188	0.035	0.40	8	12
99		b	312	197	0.021	0.32	6	10
128		b	314	296	0.050	0.53	8	14
284		b	318	901	0.625	1.35	14	22
164		b	320	369	0.406	1.43	14	20
187		b	326	421	0.062	0.74	10	16
162		b	330	327	0.416	1.40	14	20
46		b	336	107	0.005	0.08	2	6
244		b	336	691	0.239	1.33	14	20
18		b	348	52	0.046	0.19	4	8
130		b	352	284	0.232	1.19	12	20
17		b	354	41	0.670	1.78	16	20
206		b	354	475	0.250	1.51	14	20
268		b	356	777	0.168	1.40	16	16
229		b	358	622	0.240	0.95	12	16
47		b	360	116	0.184	0.95	12	16
129		b	360	257	0.034	0.29	6	10
101		b	362	228	0.545	1.59	16	24
163		b	364	332	0.126	0.82	12	14

APPENDIX C2-3

243		b	364	643	0.874	1.93	18	22
258		b	364	730	0.276	1.70	16	18
72		b	372	152	0.016	0.16	4	6
45		b	374	73	1.430	1.83	14	24
131		b	374	297	0.655	1.67	16	22
186		b	374	393	6.077	5.96	32	38
188		b	374	429	0.119	0.72	8	18
16		b	380	17	0.246	1.06	10	18
20		b	388	43	0.060	0.34	6	12
48		b	390	102	1.344	1.93	16	24
132		b	390	264	0.066	0.69	8	16
73		b	394	162	0.307	1.56	16	18
165		b	416	360	0.415	1.40	12	20
246		b	420	680	0.519	2.49	24	18
133		b	424	271	0.082	0.69	10	14
190	4	b	424	409	2.862	3.07	22	28
269		b	426	774	0.010	0.16	4	10
134		b	428	303	1.068	1.75	16	22
74		b	430	164	0.505	1.48	16	18
245		b	432	640	0.366	1.56	16	20
19		b	434	35	0.411	1.17	14	16
189		b	434	386	0.054	0.16	4	8
270		b	446	804	0.090	0.93	12	16
260		b	448	748	0.130	1.09	12	18
167		b	450	342	0.484	1.09	12	18
192		b	452	394	0.161	0.37	8	12
102		b	454	211	0.225	1.35	14	18
169		b	454	369	1.840	2.07	18	22
248		b	454	678	0.092	0.72	12	14
50		b	458	103	0.112	0.56	8	14
75		b	458	130	1.149	1.75	16	22
135		b	460	288	0.083	0.56	8	12
22		b	462	40	1.472	2.25	20	22
249		b	462	702	0.026	0.42	8	10
207		b	464	470	0.051	0.69	8	16
166		b	476	326	1.525	1.80	22	18
76		b	484	133	0.146	0.45	10	8
218		b	486	521	0.278	1.46	14	20
191		b	488	392	0.384	0.69	8	16
103		b	490	241	0.624	1.51	14	26
168		b	490	364	1.919	1.72	16	24
209		b	490	499	0.031	0.40	6	14
23		b	494	52	1.361	2.04	20	20
77		b	494	168	0.629	1.56	14	24
194		b	494	432	0.691	1.72	16	20
219		b	494	545	0.077	0.69	10	16
230		b	494	622	0.541	2.12	18	22
288		b	494	939	4.092	2.41	12	72
49		b	496	94	2.192	4.19	22	42
247		b	496	666	1.222	3.63	28	34
271		b	496	828	0.252	1.19	14	28
208		b	500	470	0.075	0.77	10	16
193		b	504	415	2.542	3.26	20	38
136	3	b	506	302	6.837	6.15	32	42

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259		b	508	707	0.115	0.87	10	16
280		b	508	886	0.633	2.15	20	20
287		b	508	923	3.070	2.62	16	54
21		b	510	17	1.457	1.83	12	26
261		b	510	745	3.251	4.16	24	36
172		b	512	380	0.177	0.50	8	12
80		b	514	186	0.761	2.04	14	34
104		b	514	222	0.508	1.51	16	18
171		b	518	348	2.230	2.46	20	24
79		b	522	175	0.199	0.69	10	16
78		b	524	134	1.045	2.15	18	22
170		b	530	325	0.062	0.29	6	8
24		b	538	44	0.232	1.01	12	16
272		b	544	810	0.100	1.01	12	16
51		b	550	110	0.114	0.56	8	14
210	2	b	554	503	2.803	3.29	20	32
289		b	566	942	0.095	0.19	4	10
137		b	570	311	0.007	0.13	2	10
196		b	576	408	0.014	0.21	4	10
173		b	580	344	0.088	0.77	8	18
250		b	582	654	0.074	0.80	12	14
53		b	584	71	0.378	1.56	14	20
138		b	584	265	0.003	0.08	2	6
197		b	588	434	0.426	1.83	16	22
55		b	592	104	0.240	1.25	12	18
290		b	594	930	0.088	0.16	4	10
174		b	596	361	0.075	0.56	6	16
25		b	600	32	0.201	1.17	16	14
54		b	610	78	0.033	0.19	4	8
140		b	618	310	0.349	1.25	12	18
251		b	618	687	0.008	0.11	2	8
81		b	620	147	0.155	0.80	12	14
52		b	622	69	0.011	0.08	2	6
195		b	622	392	0.282	1.35	16	16
105		b	624	208	0.020	0.16	4	6
231		b	624	626	0.017	0.16	4	8
291		b	628	946	0.803	0.82	8	30
139		b	630	292	0.399	1.19	12	20
211		b	636	454	0.848	2.12	18	26
212		b	638	503	0.105	0.58	10	12
84		b	640	162	0.261	1.01	12	16
176		b	640	351	1.385	2.36	18	24
56		b	642	104	1.056	2.41	20	24
293		b	642	929	0.059	0.13	2	10
85		b	644	185	0.029	0.16	2	12
220		b	648	519	0.159	0.90	14	12
263		b	648	760	3.307	5.86	38	32
252		b	650	641	0.018	0.13	2	10
213		b	652	477	0.173	0.87	14	10
26		b	654	17	0.995	1.99	10	38
27		b	656	45	1.206	1.86	14	26
175		b	656	320	1.309	2.76	20	32
262		b	656	707	0.317	1.06	10	20
28		b	660	63	0.974	2.01	14	30

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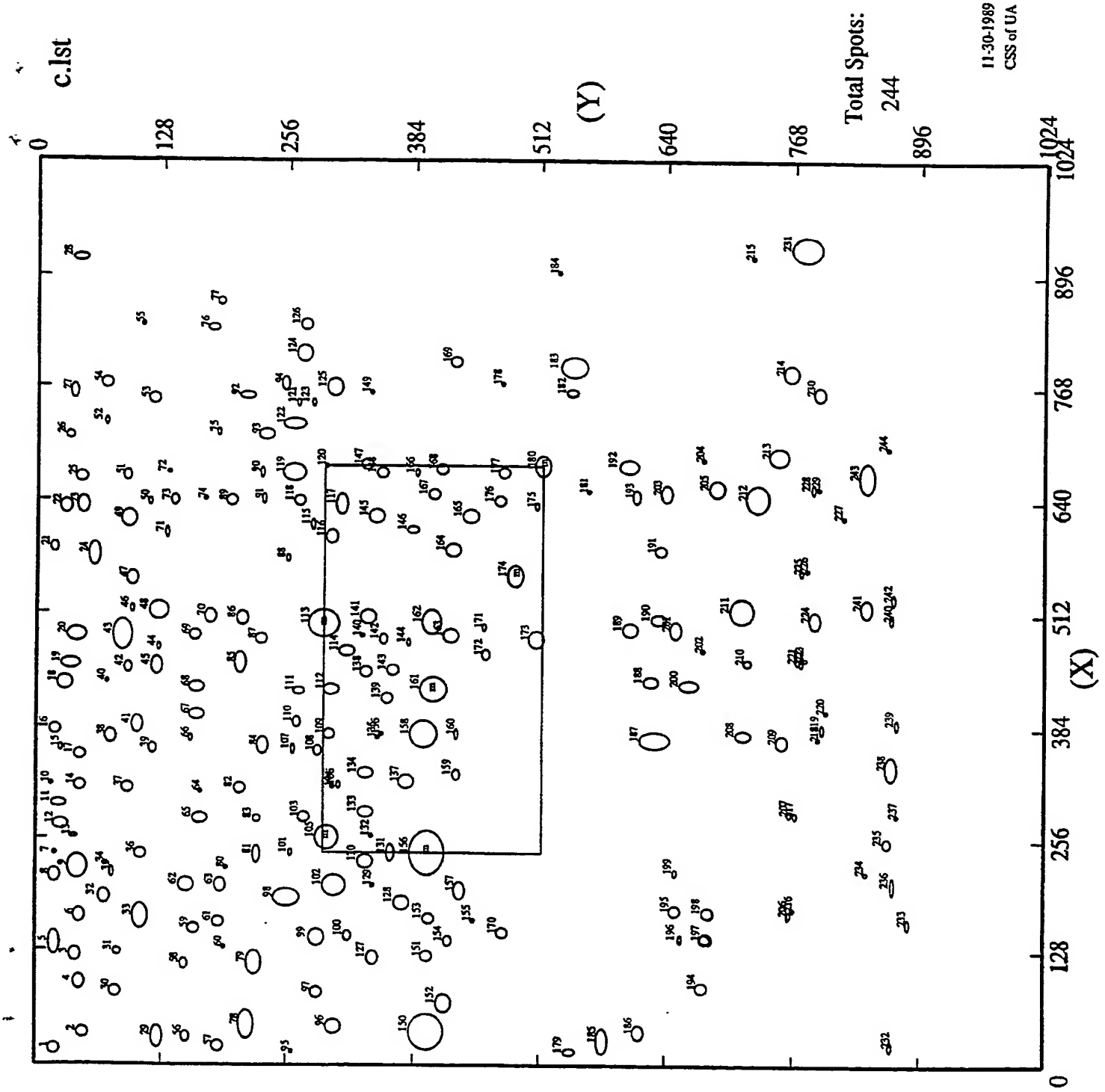
82		b	662	128	0.397	1.30	12	20
106		b	662	207	0.569	1.86	14	28
292		b	662	903	1.130	2.62	16	34
141		b	664	278	0.672	1.78	16	26
221		b	666	530	0.021	0.16	4	8
83		b	668	154	0.271	1.06	12	20
107		b	668	240	0.327	1.54	12	24
198		b	668	415	0.514	2.01	20	20
275		b	704	793	0.012	0.08	2	6
34		b	706	63	0.089	0.34	6	12
273		b	708	783	0.013	0.08	2	6
142		b	712	271	1.590	3.90	26	24
178		b	712	357	2.703	4.64	36	34
274		b	712	789	0.023	0.13	2	10
222	1	b	714	521	2.609	4.35	30	26
232		b	714	615	0.577	2.25	24	20
87		b	716	162	0.310	1.14	12	18
88		b	716	191	0.143	0.61	6	20
32		b	718	36	0.545	1.06	8	26
144		b	718	301	0.461	1.19	10	22
214		b	718	473	0.405	1.96	18	22
199		b	720	391	0.167	0.87	10	16
30		b	722	16	0.625	1.01	8	22
57		b	722	104	0.641	1.25	14	22
294		b	722	930	0.695	1.01	8	28
110		b	724	238	0.154	0.56	8	16
200		b	724	440	0.033	0.32	8	8
58		b	726	124	0.441	1.19	12	20
109		b	726	215	0.012	0.08	2	6
143		b	748	282	0.032	0.16	4	6
277		b	748	827	0.244	1.22	14	16
31		b	750	34	0.097	0.34	8	8
177		b	750	321	0.037	0.24	6	8
253		b	756	641	0.004	0.08	2	6
255		b	756	649	0.005	0.08	2	6
111		b	758	239	0.371	1.22	14	16
233		b	760	633	0.056	0.56	10	12
254		b	762	644	0.010	0.16	4	6
86		b	764	130	0.111	0.64	12	12
276		b	764	800	0.851	2.76	22	28
29		b	766	14	0.034	0.16	4	6
33		b	766	45	0.163	0.66	14	10
108		b	766	193	0.197	1.19	14	16
223		b	768	550	0.662	3.45	28	24
146		b	770	268	2.464	3.31	28	22
147		b	770	308	0.196	1.03	12	16
179		b	770	361	0.004	0.11	2	8
60		b	774	89	0.210	1.03	12	16
295		b	780	939	4.609	3.05	24	52
89		b	802	129	0.419	1.93	18	22
112		b	802	201	0.385	1.64	18	22
215		b	802	478	0.065	0.87	12	12
36		b	804	52	0.366	1.96	16	24
35		b	806	16	0.418	1.19	8	26

148	b	812	309	0.508	2.25	18	22
145	b	816	263	0.108	0.50	10	10
224	b	818	561	1.720	3.50	26	24
59	b	826	82	0.324	1.19	12	18
264	b	834	747	0.005	0.08	2	6
201	b	836	431	0.340	1.59	16	18
114	b	844	230	0.177	1.14	14	14
151	b	844	319	0.002	0.08	2	6
180	b	844	368	0.041	0.72	12	12
225	b	844	537	0.004	0.08	2	6
62	b	846	104	0.008	0.16	4	6
90	b	846	131	0.003	0.08	2	6
149	b	846	276	2.246	2.78	22	24
61	b	876	91	0.010	0.08	2	6
113	b	880	195	0.277	1.35	16	16
150	b	880	284	0.761	1.75	18	20
226	b	880	543	0.134	1.38	20	14
234	b	880	597	0.004	0.08	2	6
181	b	884	371	0.080	0.66	10	12
281	b	898	858	3.317	4.53	34	28
116	b	912	210	0.858	2.23	22	18
117	b	912	255	0.187	0.66	10	14
256	b	912	648	0.247	1.03	16	12
227	b	920	559	1.290	2.60	26	18
152	b	926	294	0.283	0.80	12	12
63	b	928	88	8.211	8.08	54	32
236	b	930	609	0.033	0.08	2	6
257	b	936	666	0.091	0.19	4	10
235	b	946	594	2.900	3.26	20	36
115	b	950	203	0.894	2.36	22	18



APPENDIX C3-1

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Spotlist for 'c'. Image size 1024 x 1024. 244 spots.

Rec	Spotname	Image	X	Y	II	Area	Ht	Wd
95		c	16	261	0.010	0.08	2	6
179		c	18	541	0.126	0.80	14	10
1		c	20	18	0.346	0.82	12	14
57		c	22	186	0.217	1.25	12	18
232		c	24	868	0.123	0.34	4	18
185		c	28	576	0.550	2.76	16	30
29		c	32	124	1.842	2.33	16	26
56		c	34	153	0.191	1.09	10	18
2		c	36	47	0.674	1.38	14	18
150		c	38	397	8.544	7.47	38	42
186		c	38	613	0.187	1.38	14	20
96		c	44	305	0.879	1.86	18	20
78		c	46	216	2.559	3.34	20	36
152		c	70	415	1.606	2.09	20	24
30		c	82	80	0.156	1.09	12	18
97		c	82	288	0.219	1.22	14	16
194		c	88	676	0.097	1.06	12	18
4		c	92	44	1.188	1.78	16	20
58		c	112	151	0.040	0.69	10	14
79		c	116	223	1.811	2.73	18	30
127		c	120	343	0.294	1.46	14	20
3		c	124	40	1.087	1.56	16	20
151		c	124	398	0.166	1.17	12	18
31		c	126	83	0.066	0.58	10	12
60		c	132	191	0.002	0.11	2	8
5		c	136	18	1.597	2.01	14	28
154		c	140	419	0.117	0.82	10	16
99		c	144	286	1.450	2.46	20	22
196		c	144	654	0.043	0.56	8	12
197		c	144	681	0.118	1.11	14	14
100		c	146	318	0.162	1.03	10	18
170		c	150	475	0.219	1.17	14	16
59		c	154	160	0.111	0.93	12	16
61		c	162	185	0.133	1.06	14	16
233		c	162	884	0.238	0.48	4	18
155		c	164	445	0.004	0.11	2	8
153		c	166	400	0.333	1.43	16	18
6		c	168	44	0.856	1.59	14	20
33		c	168	107	0.591	3.47	20	32
206		c	172	764	0.009	0.21	4	10
198		c	174	682	0.187	1.40	16	16
195		c	176	648	0.090	1.03	12	16
216		c	178	769	0.003	0.11	2	8
128		c	184	373	0.954	1.91	18	20
32		c	188	68	0.611	1.46	16	20
98		c	190	257	1.171	2.97	32	24
157		c	198	432	0.603	1.70	16	22
63		c	202	187	0.259	1.40	14	20
102		c	202	305	2.703	3.74	28	26

APPENDIX C3-2

62		c	204	153	0.677	1.96	18	20
129		c	204	343	0.020	0.11	2	8
236		c	206	869	0.583	0.90	8	22
8		c	214	19	0.891	1.33	14	20
35		c	216	78	0.118	0.69	8	16
199		c	218	650	0.020	0.45	8	12
234		c	220	841	0.007	0.08	2	6
9		c	222	41	3.174	3.26	22	28
80		c	222	193	0.010	0.11	2	8
34		c	228	72	0.021	0.16	4	6
130		c	230	336	1.279	2.01	18	20
7		c	238	18	0.124	0.40	8	8
36		c	238	105	0.114	0.85	12	14
81		c	238	225	0.142	0.87	10	22
101		c	242	260	0.059	0.45	8	10
131		c	242	361	0.486	1.11	10	22
156	6	c	242	397	9.890	9.94	36	54
235		c	254	863	0.329	0.72	10	18
13		c	258	39	0.176	0.53	10	8
105	5	c	258	297	2.975	3.90	26	34
132		c	260	341	0.013	0.08	2	6
12		c	272	25	1.544	1.88	18	18
65		c	280	167	0.254	1.35	18	18
83		c	280	225	0.030	0.53	10	10
103		c	282	275	0.366	1.22	14	18
217		c	286	770	0.013	0.27	4	12
237		c	286	873	0.038	0.08	2	6
133		c	288	336	0.707	1.93	20	18
207		c	288	764	0.009	0.21	4	12
11		c	296	23	0.581	1.25	18	12
64		c	310	167	0.004	0.08	2	6
37		c	312	93	0.394	1.33	14	18
82		c	312	207	0.123	1.09	14	14
14		c	314	45	0.242	0.95	12	16
104		c	316	303	0.006	0.08	2	6
10		c	318	15	0.012	0.08	2	6
106		c	318	308	0.019	0.24	4	10
137		c	320	377	0.582	1.70	18	20
159		c	328	427	0.060	0.72	10	14
134		c	330	335	0.608	1.80	18	18
238		c	338	867	1.230	1.88	14	28
17		c	350	43	0.376	1.30	14	16
108		c	356	288	0.155	0.66	10	18
15		c	358	24	0.054	0.24	4	10
39		c	358	119	0.133	0.90	10	16
107		c	358	261	0.049	0.40	6	14
84		c	362	232	0.337	1.64	16	22
209		c	368	756	0.142	1.22	14	20
66		c	370	157	0.038	0.32	6	10
187		c	370	627	0.998	3.26	34	24
38		c	372	75	0.926	1.59	14	20
135		c	372	347	0.012	0.11	2	8
218		c	372	793	0.002	0.08	2	6
109		c	374	300	0.403	1.54	16	18

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160		c	374	428	0.121	0.77	8	18
136		c	376	352	0.026	0.16	4	8
158		c	376	393	5.207	5.86	30	36
208		c	376	717	0.224	1.78	18	18
16		c	380	19	0.416	1.51	16	18
219		c	382	796	0.010	0.24	4	16
41		c	386	103	1.062	1.93	16	22
110		c	390	265	0.071	0.64	10	14
239		c	390	873	0.251	0.48	6	16
67		c	396	163	0.325	1.70	18	16
220		c	402	801	0.001	0.11	2	8
139		c	416	358	0.485	1.43	16	16
111		c	424	269	0.100	0.77	12	12
112		c	426	301	0.747	1.78	18	18
161	4	c	426	404	4.198	4.06	30	28
68		c	428	163	0.522	1.56	18	16
18		c	432	28	1.093	1.86	20	20
200		c	432	663	0.281	1.75	22	16
40		c	434	71	0.008	0.08	2	6
188		c	436	623	0.232	1.54	18	16
138		c	446	336	0.427	1.11	12	16
143		c	448	363	0.519	1.22	14	14
42		c	450	93	0.192	0.85	10	14
45		c	452	122	1.144	1.93	16	22
19		c	454	34	1.594	1.99	22	18
85		c	456	208	0.417	1.88	14	26
210		c	458	721	0.046	0.58	10	12
222		c	458	776	0.015	0.24	4	12
221		c	460	771	0.006	0.13	2	10
223		c	462	779	0.004	0.08	2	6
172		c	464	457	0.067	0.66	10	14
114		c	470	316	1.003	1.35	18	16
202		c	472	677	0.004	0.08	2	6
44		c	474	124	0.170	0.37	8	10
144		c	480	379	0.165	0.24	6	10
87		c	484	229	0.431	1.14	14	16
142		c	484	353	0.659	0.98	10	18
173		c	484	508	0.413	1.91	18	22
20		c	486	40	1.542	2.15	22	20
69		c	486	161	0.465	1.25	14	18
140		c	486	333	0.172	0.29	6	8
43		c	488	87	2.068	3.18	22	38
163		c	488	421	0.904	1.88	18	20
189		c	496	603	0.451	2.04	20	20
201		c	496	649	0.258	1.19	12	22
171		c	498	455	0.029	0.37	6	12
113	3	c	500	294	5.686	5.70	34	36
162		c	502	402	2.658	3.58	22	34
86		c	506	209	0.535	1.46	14	20
190		c	506	632	0.456	1.62	20	18
224		c	506	790	0.251	1.38	14	24
70		c	508	177	0.465	1.40	14	20
141		c	508	337	1.218	1.86	18	20
240		c	510	867	0.105	0.24	2	18

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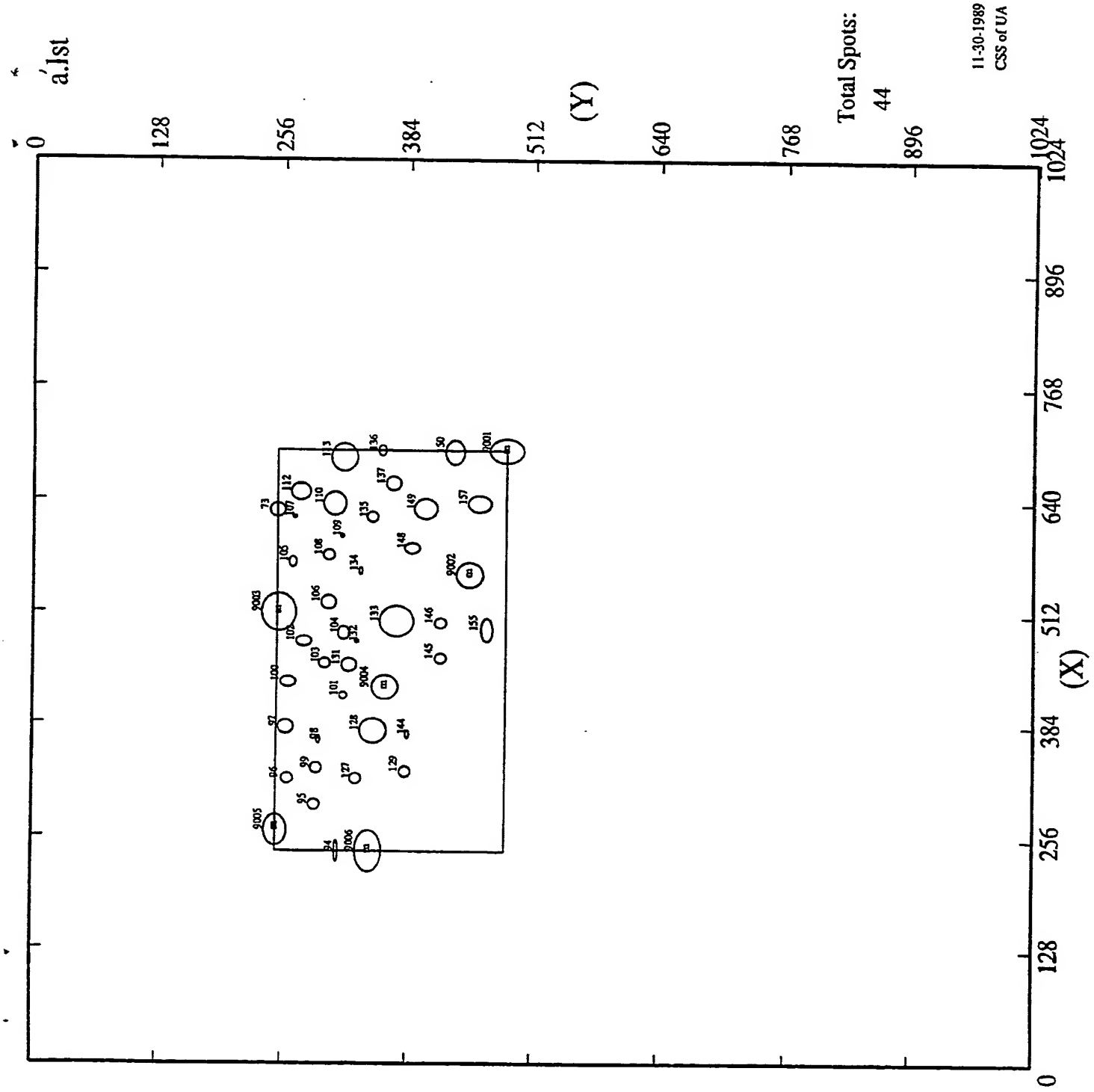
48		c	514	124	1.419	2.60	22	22
211		c	516	715	3.561	4.64	26	34
46		c	518	96	0.115	0.48	8	10
241		c	520	843	0.462	1.43	14	22
242		c	530	870	0.196	0.37	4	16
47		c	550	97	0.247	0.98	14	20
174	2	c	554	486	1.703	2.62	20	26
225		c	560	776	0.012	0.27	4	12
226		c	562	782	0.009	0.16	4	8
88		c	574	255	0.024	0.32	6	10
24		c	578	58	0.701	2.09	16	32
164		c	582	423	0.402	1.88	18	20
191		c	584	634	0.062	0.80	12	14
21		c	586	16	0.174	0.85	10	18
116		c	600	301	0.425	1.43	14	20
71		c	602	132	0.081	0.56	8	14
146		c	606	382	0.114	0.85	12	12
115		c	612	282	0.136	0.48	8	14
49		c	618	94	0.835	2.20	20	22
145		c	622	346	1.103	2.04	20	20
165		c	622	440	0.462	1.80	18	20
227		c	622	817	0.006	0.08	2	6
22		c	632	29	0.792	1.70	14	20
23		c	634	46	0.533	1.14	12	22
175		c	634	508	0.062	0.42	8	10
117		c	636	310	0.713	1.83	16	26
50		c	638	115	0.128	0.53	8	12
73		c	640	139	0.232	0.95	10	18
89		c	640	198	0.265	1.11	12	16
118		c	640	268	0.477	1.27	16	16
176		c	640	470	0.289	1.27	14	18
74		c	642	171	0.013	0.08	2	6
91		c	642	232	0.122	0.56	8	14
212		c	644	732	2.036	4.51	26	36
193		c	646	609	0.165	0.90	10	20
167		c	648	403	0.286	1.17	14	18
203		c	650	640	0.238	1.43	12	22
181		c	652	559	0.007	0.08	2	6
205		c	656	690	0.601	2.28	20	22
228		c	656	787	0.125	0.69	8	16
229		c	656	793	0.015	0.11	2	8
25		c	668	44	0.314	0.90	12	18
51		c	670	91	0.147	0.69	10	14
243		c	670	841	1.672	3.02	18	40
72		c	672	133	0.038	0.29	6	8
148		c	672	352	0.360	1.62	16	18
90		c	674	228	0.108	0.48	8	14
119		c	674	263	1.041	3.18	26	22
166		c	674	386	0.076	0.48	8	12
177		c	674	475	0.148	1.01	12	18
168		c	678	412	0.131	0.72	12	16
120		c	680	295	0.012	0.08	2	6
180	1	c	682	514	1.216	2.86	20	26
192		c	682	599	0.462	2.25	22	20

APPENDIX C3-5

147	c	684	336	0.232	1.14	14	16
204	c	688	677	0.008	0.08	2	6
213	c	692	753	0.661	2.17	22	22
244	c	702	863	0.051	0.11	2	8
26	c	714	31	0.092	0.50	10	10
93	c	716	233	0.473	1.46	18	16
75	c	718	184	0.024	0.21	4	10
122	c	728	262	0.915	2.07	24	18
52	c	730	68	0.057	0.42	8	12
121	c	752	266	0.085	0.45	8	10
123	c	752	280	0.082	0.42	8	10
53	c	756	118	0.124	1.03	12	18
92	c	760	213	0.149	1.25	18	12
27	c	762	36	0.109	0.66	10	20
230	c	762	793	0.223	1.72	14	20
149	c	764	339	0.002	0.08	2	6
182	c	764	542	0.171	0.77	16	10
125	c	768	303	0.575	2.04	18	22
54	c	774	68	0.109	0.87	12	14
94	c	774	253	0.157	0.77	10	20
178	c	774	472	0.006	0.19	4	8
214	c	788	764	0.279	1.88	18	22
183	c	792	543	2.582	4.24	32	26
169	c	798	426	0.147	1.22	16	16
124	c	808	272	1.450	2.17	20	22
76	c	838	178	0.071	0.90	12	12
55	c	842	107	0.003	0.08	2	6
126	c	842	274	0.531	1.62	16	18
77	c	866	186	0.043	0.56	10	10
184	c	900	528	0.029	0.16	4	6
28	c	916	41	0.157	0.95	18	10
215	c	918	726	0.021	0.16	4	6
231	c	928	779	2.920	4.85	34	28



APPENDIX C4-1

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Filename: a.att

Rec#	X	Y	NewX	NewY	PI	MW	II	Area	Ht	Wd
9001	696	484	696	484	-1.00	19.00	3.652	5.140	36	28
136	696	357	696	357	-1.00	21.76	0.300	1.030	10	18
150	694	430	694	430	-1.02	20.61	1.023	2.620	22	30
113	690	319	690	319	-1.05	24.20	3.868	5.060	32	36
137	658	369	658	369	-1.28	21.39	0.859	1.990	20	20
112	650	274	650	274	-1.33	26.68	1.391	1.670	22	22
110	636	308	636	308	-1.43	24.81	2.391	3.340	24	30
157	636	457	636	457	-1.43	20.02	1.162	2.200	28	24
149	630	402	630	402	-1.48	20.97	1.845	2.860	24	26
73	628	250	628	250	-1.49	28.00	1.006	1.800	20	20
107	620	268	620	268	-1.55	27.01	0.049	0.190	4	8
135	620	348	620	348	-1.55	22.54	0.281	1.140	14	16
109	600	316	600	316	-1.69	24.37	0.022	0.190	4	8
148	586	389	586	389	-1.79	21.13	0.264	1.540	18	16
108	576	302	576	302	-1.86	25.14	0.111	1.090	12	18
105	570	265	570	265	-1.90	27.18	0.052	0.720	10	14
134	560	336	560	336	-1.98	23.27	0.055	0.480	8	12
9002	556	447	556	447	-2.00	20.39	4.757	5.120	32	32
106	524	302	524	302	-2.18	25.14	1.773	2.330	20	20
9003	512	252	512	252	-2.24	27.89	8.928	6.710	38	46
133	504	372	504	372	-2.32	21.35	3.676	5.800	36	38
146	500	417	500	417	-2.35	20.78	0.203	1.300	14	18
155	492	464	492	464	-2.42	19.76	0.379	1.910	16	32
104	490	319	490	319	-2.44	24.20	1.404	1.380	14	20
132	480	333	480	333	-2.53	23.43	0.039	0.080	2	6
102	478	277	478	277	-2.55	26.52	1.250	1.540	20	16
145	460	417	460	417	-2.70	20.78	0.140	1.140	14	16
103	454	298	454	298	-2.76	25.36	0.437	0.980	12	16
131	452	324	452	324	-2.78	23.93	1.888	2.170	20	20
100	432	261	432	261	-2.95	27.40	0.884	1.910	18	18
9004	426	360	426	360	-3.00	21.50	4.162	3.900	32	28
101	416	317	416	317	-3.07	24.31	0.131	0.610	10	12
97	380	259	380	259	-3.29	27.51	0.702	1.960	20	20
128	376	349	376	349	-3.31	22.46	3.781	5.190	30	32
144	372	385	372	385	-3.34	21.19	0.051	0.370	6	12
98	366	294	366	294	-3.38	25.58	0.026	0.270	4	10
99	334	291	334	291	-3.57	25.75	0.162	1.110	14	14
129	332	382	332	382	-3.59	21.22	0.074	0.930	12	14
127	324	332	324	332	-3.63	23.49	0.191	1.300	12	18
96	322	261	322	261	-3.65	27.40	0.150	0.980	16	14
95	292	290	292	290	-3.83	25.80	0.296	1.540	16	18
9005	264	250	264	250	-4.00	28.00	3.127	4.590	26	38
9006	240	346	240	346	-4.21	22.71	7.771	7.790	32	52
94	240	312	240	312	-4.21	24.59	0.531	1.190	8	26

Print file name: a.als, Time: 15:19 Date: 12/1/1989 Page:

Filename: a.als
Window = X : 240 ~ 696
Y : 250 ~ 484

Rec#	Spotname	Image	NewX	NewY	II	Area	Ht	Wd
9001	1	a	696	484	3.652	5.140	36	28
136		a	696	357	0.300	1.030	10	18
150		a	694	430	1.023	2.620	22	30
113		a	690	319	3.868	5.060	32	36
137		a	658	369	0.859	1.990	20	20
112		a	650	274	1.391	1.670	22	22
110		a	636	308	2.391	3.340	24	30
157		a	636	457	1.162	2.200	28	24
149		a	630	402	1.845	2.860	24	26
73		a	628	250	1.006	1.800	20	20
107		a	620	268	0.049	0.190	4	8
135		a	620	348	0.281	1.140	14	16
109		a	600	316	0.022	0.190	4	8
148		a	586	389	0.264	1.540	18	16
108		a	576	302	0.111	1.090	12	18
105		a	570	265	0.052	0.720	10	14
134		a	560	336	0.055	0.480	8	12
9002	2	a	556	447	4.757	5.120	32	32
106		a	524	302	1.773	2.330	20	20
9003	3	a	512	252	8.928	6.710	38	46
133		a	504	372	3.676	5.800	36	38
146		a	500	417	0.203	1.300	14	18
155		a	492	464	0.379	1.910	16	32
104		a	490	319	1.404	1.380	14	20
132		a	480	333	0.039	0.080	2	6
102		a	478	277	1.250	1.540	20	16
145		a	460	417	0.140	1.140	14	16
103		a	454	298	0.437	0.980	12	16
131		a	452	324	1.888	2.170	20	20
100		a	432	261	0.884	1.910	18	18
9004	4	a	426	360	4.162	3.900	32	28
101		a	416	317	0.131	0.610	10	12
97		a	380	259	0.702	1.960	20	20
128		a	376	349	3.781	5.190	30	32
144		a	372	385	0.051	0.370	6	12
98		a	366	294	0.026	0.270	4	10
99		a	334	291	0.162	1.110	14	14
129		a	332	382	0.074	0.930	12	14
127		a	324	332	0.191	1.300	12	18
96		a	322	261	0.150	0.980	16	14
95		a	292	290	0.296	1.540	16	18
9005	5	a	264	250	3.127	4.590	26	38
9006	6	a	240	346	7.771	7,790	32	52
94		a	240	312	0.531	1,190	8	26

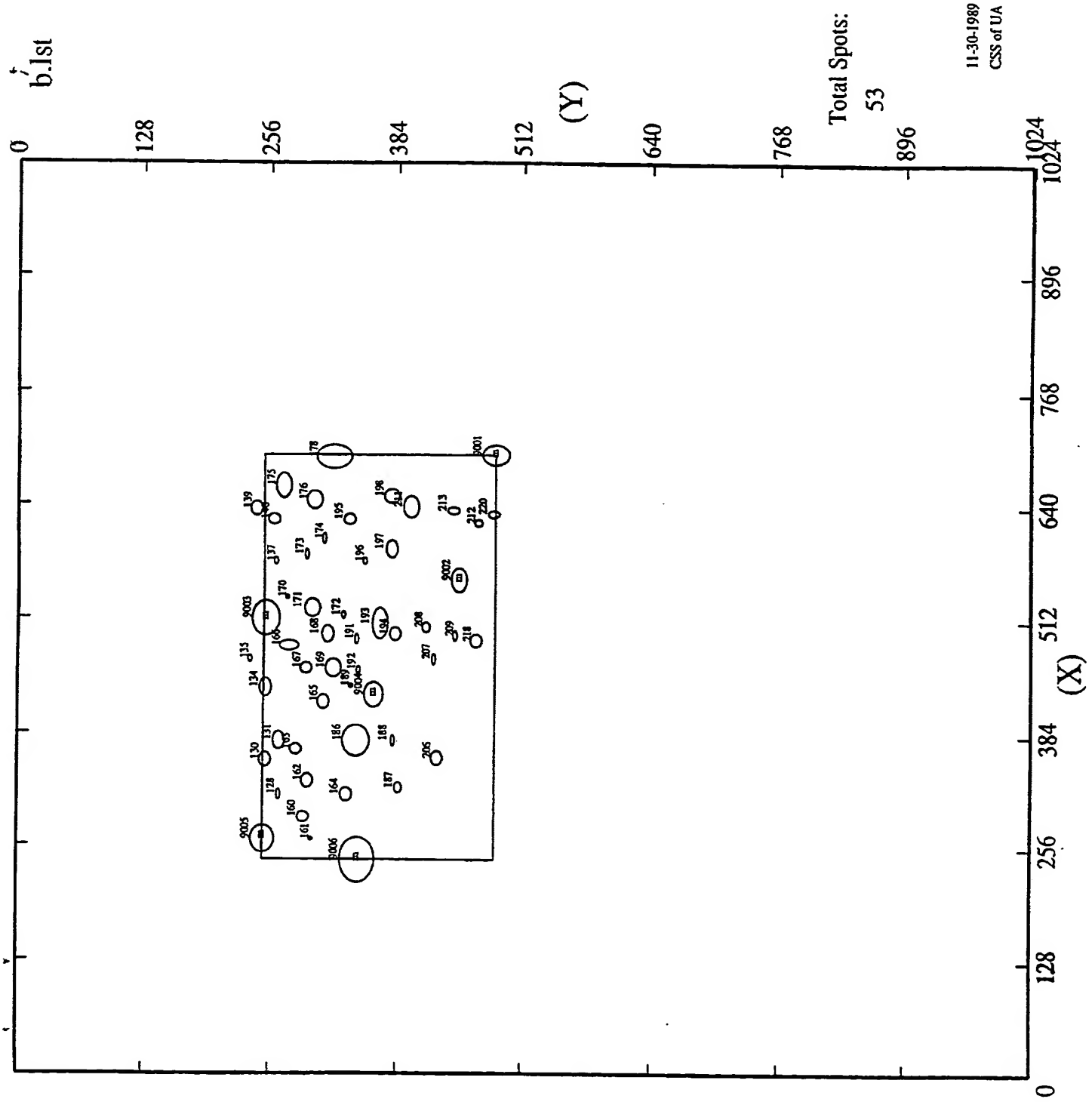
APPENDIX C4-3

Print file name: a.mks, Time: 15:18 Date: 12/1/1989 Page:

a.mks
Window = X : 240 ~ 696
Y : 250 ~ 484

---------- 6 Markers ----------

Marker_name	X	Y
9001	696	484
9002	556	447
9003	512	252
9004	426	360
9005	264	250
9006	240	346



APPENDIX C5-1

Print file name: b.att, Time: 15:14 Date: 12/1/1989 Page:

Filename: b.att

Rec#	X	Y	NewX	NewY	PI	MW	II	Area	Ht	Wd
9001	714	521	696	484	-1.00	19.00	2.609	4.350	30	26
178	712	357	694	320	-1.02	24.15	2.703	4.640	36	34
198	668	415	650	378	-1.33	21.28	0.514	2.010	20	20
175	656	320	662	270	-1.25	26.90	1.309	2.760	20	32
213	652	477	634	440	-1.45	20.48	0.173	0.870	14	10
220	648	519	630	482	-1.48	19.08	0.159	0.900	14	12
176	640	351	646	301	-1.36	25.19	1.385	2.360	18	24
212	638	503	620	466	-1.55	19.68	0.105	0.580	10	12
211	636	454	638	398	-1.42	21.02	0.848	2.120	18	26
139	630	292	636	242	-1.43	27.56	0.399	1.190	12	20
195	622	392	624	336	-1.52	23.27	0.282	1.350	16	16
140	618	310	624	260	-1.52	27.45	0.349	1.250	12	18
174	596	361	602	311	-1.68	24.64	0.075	0.560	6	16
197	588	434	590	378	-1.76	21.28	0.426	1.830	16	22
173	580	344	586	294	-1.79	25.58	0.088	0.770	8	18
196	576	408	578	352	-1.85	22.20	0.014	0.210	4	10
137	570	311	576	261	-1.86	27.40	0.007	0.130	2	10
9002	554	503	556	447	-2.00	20.39	2.803	3.290	20	32
170	530	325	536	275	-2.11	26.63	0.062	0.290	6	8
171	518	348	524	298	-2.18	25.36	2.230	2.460	20	24
172	512	380	518	330	-2.21	23.60	0.177	0.500	8	12
9003	506	302	512	252	-2.24	27.89	6.837	6.150	32	42
193	504	415	506	366	-2.30	21.43	2.542	3.260	20	38
208	500	470	502	414	-2.33	20.82	0.075	0.770	10	16
194	494	432	496	383	-2.39	21.21	0.691	1.720	16	20
209	490	499	492	443	-2.42	20.45	0.031	0.400	6	14
168	490	364	496	314	-2.39	24.48	1.919	1.720	16	24
191	488	392	490	343	-2.44	22.88	0.384	0.690	8	16
218	486	521	488	465	-2.46	19.72	0.278	1.460	14	20
166	476	326	482	276	-2.51	26.57	1.525	1.800	22	18
207	464	470	466	421	-2.65	20.73	0.051	0.690	8	16
135	460	288	466	238	-2.65	27.34	0.083	0.560	8	12
169	454	369	456	320	-2.74	24.15	1.840	2.070	18	22
192	452	394	454	345	-2.76	22.77	0.161	0.370	8	12
167	450	342	456	292	-2.74	25.69	0.484	1.090	12	18
189	434	386	436	337	-2.92	23.21	0.054	0.160	4	8
134	428	303	434	253	-2.93	27.84	1.068	1.750	16	22
9004	424	409	426	360	-3.00	21.50	2.862	3.070	22	28
165	416	360	418	311	-3.05	24.64	0.415	1.400	12	20
188	374	429	376	380	-3.31	21.25	0.119	0.720	8	18
186	374	393	376	344	-3.31	22.83	6.077	5.960	32	38
131	374	297	376	266	-3.31	27.12	0.655	1.670	16	22
163	364	332	366	283	-3.38	26.19	0.126	0.820	12	14
206	354	475	356	426	-3.44	20.66	0.250	1.510	14	20
130	352	284	354	253	-3.45	27.84	0.232	1.190	12	20
162	330	327	332	296	-3.59	25.47	0.416	1.400	14	20
187	326	421	322	386	-3.65	21.17	0.062	0.740	10	16
164	320	369	316	334	-3.68	23.38	0.406	1.430	14	20
128	314	296	316	265	-3.68	27.18	0.050	0.530	8	14
160	288	322	290	291	-3.84	25.75	0.489	1.560	16	18
9005	262	281	264	250	-4.00	28.00	4.348	4.350	26	36

APPENDIX C5-2

Print file name: b.att, Time: 15:14 Date: 12/1/1989 Page:

161	262	330	264	299	-4.00	25.30	0.035	0.190	4	8
9006	244	381	240	346	-4.21	22.71	11.183	9.490	40	54

APPENDIX C5-3

Print file name: b.als, Time: 15:20 Date: 12/1/1989 Page:

Filename: b.als
Window = X : 244 ~ 714
Y : 281 ~ 521

Rec#	Spotname	Image	NewX	NewY	II	Area	Ht	Wd
9001	1	b	696	484	2.609	4.350	30	26
178		b	694	320	2.703	4.640	36	34
198		b	650	378	0.514	2.010	20	20
175		b	662	270	1.309	2.760	20	32
213		b	634	440	0.173	0.870	14	10
220		b	630	482	0.159	0.900	14	12
176		b	646	301	1.385	2.360	18	24
212		b	620	466	0.105	0.580	10	12
211		b	638	398	0.848	2.120	18	26
139		b	636	242	0.399	1.190	12	20
195		b	624	336	0.282	1.350	16	16
140		b	624	260	0.349	1.250	12	18
174		b	602	311	0.075	0.560	6	16
197		b	590	378	0.426	1.830	16	22
173		b	586	294	0.088	0.770	8	18
196		b	578	352	0.014	0.210	4	10
137		b	576	261	0.007	0.130	2	10
9002	2	b	556	447	2.803	3.290	20	32
170		b	536	275	0.062	0.290	6	8
171		b	524	298	2.230	2.460	20	24
172		b	518	330	0.177	0.500	8	12
9003	3	b	512	252	6.837	6.150	32	42
193		b	506	366	2.542	3.260	20	38
208		b	502	414	0.075	0.770	10	16
194		b	496	383	0.691	1.720	16	20
209		b	492	443	0.031	0.400	6	14
168		b	496	314	1.919	1.720	16	24
191		b	490	343	0.384	0.690	8	16
218		b	488	465	0.278	1.460	14	20
166		b	482	276	1.525	1.800	22	18
207		b	466	421	0.051	0.690	8	16
135		b	466	238	0.083	0.560	8	12
169		b	456	320	1.840	2.070	18	22
192		b	454	345	0.161	0.370	8	12
167		b	456	292	0.484	1.090	12	18
189		b	436	337	0.054	0.160	4	8
134		b	434	253	1.068	1.750	16	22
9004	4	b	426	360	2.862	3.070	22	28
165		b	418	311	0.415	1.400	12	20
188		b	376	380	0.119	0.720	8	18
186		b	376	344	6.077	5.960	32	38
131		b	376	266	0.655	1.670	16	22
163		b	366	283	0.126	0.820	12	14
206		b	356	426	0.250	1.510	14	20
130		b	354	253	0.232	1.190	12	20
162		b	332	296	0.416	1.400	14	20
187		b	322	386	0.062	0.740	10	16
164		b	316	334	0.406	1.430	14	20
128		b	316	265	0.050	0.530	8	14

APPENDIX C5-4

Print file name: b.als, Time: 15:20 Date: 12/1/1989 Page:

160	b	290	291	0.489	1.560	16	18
9005 5	b	264	250	4.348	4.350	26	36
161	b	264	299	0.035	0.190	4	8
9006 6	b	240	346	11.183	9.490	40	54

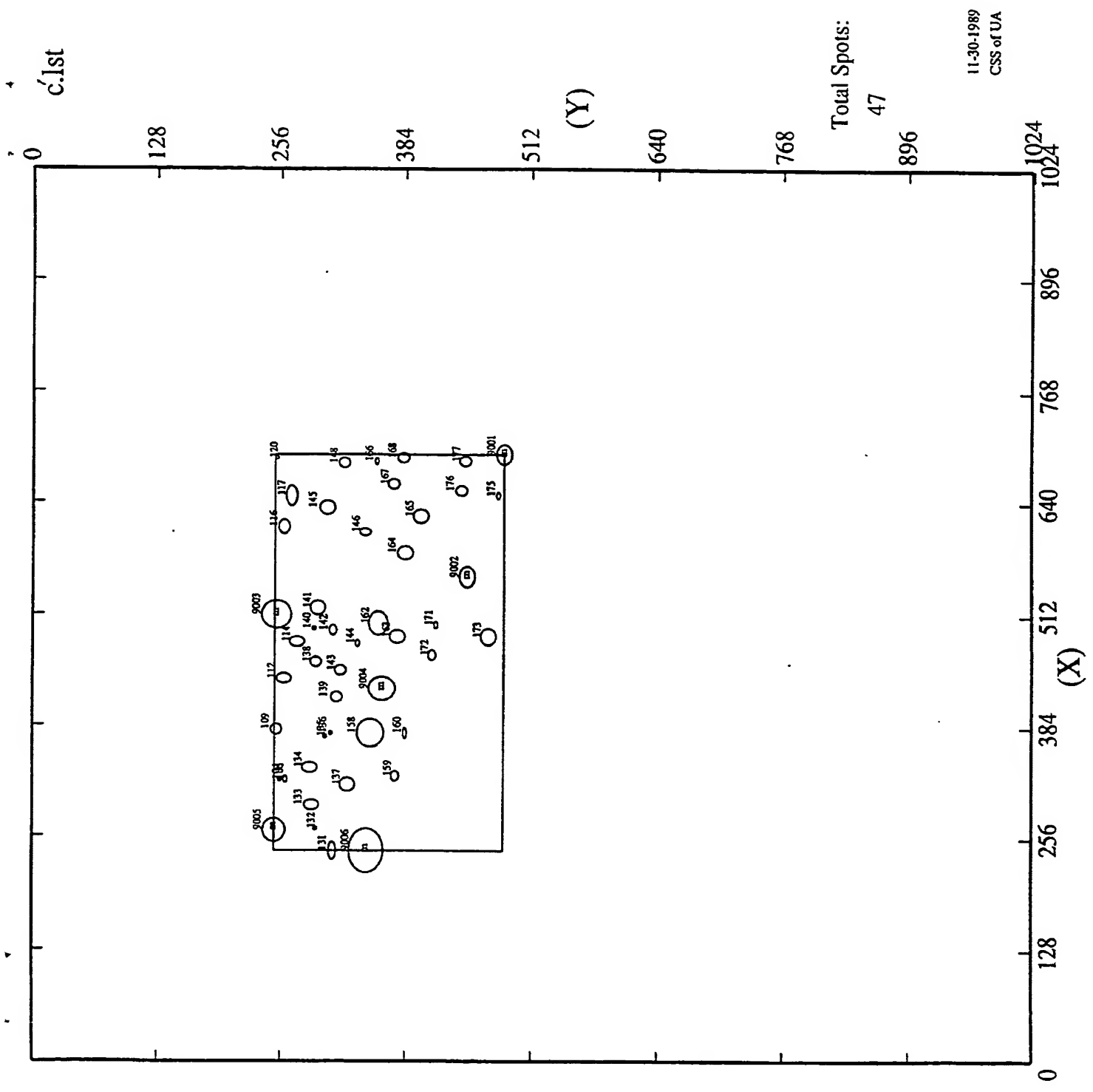
APPENDIX C5-5

Print file name: b.mks, Time: 15:19 Date: 12/1/1989 Page:

b.mks
Window = X : 244 ~ 714
Y : 281 ~ 521

---------- 6 Markers ----------

Marker_name	X	Y
9001	714	521
9002	554	503
9003	506	302
9004	424	409
9005	262	281
9006	244	381



APPENDIX C6-1

Print file name: c.att, Time: 15:15 Date: 12/1/1989 Page:

Filename: c.att

Rec#	X	Y	NewX	NewY	PI	MW	II	Area	Ht	Wd
9001	682	514	696	484	-1.00	19.00	1.216	2.860	20	26
120	680	295	692	253	-1.03	27.84	0.012	0.080	2	6
168	678	412	692	382	-1.03	21.22	0.131	0.720	12	16
177	674	475	688	445	-1.06	20.42	0.148	1.010	12	18
166	674	386	688	356	-1.06	21.85	0.076	0.480	8	12
148	672	352	686	322	-1.08	24.04	0.360	1.620	16	18
167	648	403	662	373	-1.25	21.34	0.286	1.170	14	18
176	640	470	654	440	-1.30	20.48	0.289	1.270	14	18
117	636	310	648	268	-1.35	27.01	0.713	1.830	16	26
175	634	508	648	478	-1.35	19.23	0.062	0.420	8	10
145	622	346	634	304	-1.45	25.03	1.103	2.040	20	20
165	622	440	624	401	-1.52	20.98	0.462	1.800	18	20
146	606	382	608	343	-1.63	22.88	0.114	0.850	12	12
116	600	301	612	259	-1.60	27.51	0.425	1.430	14	20
164	582	423	584	384	-1.80	21.20	0.402	1.880	18	20
9002	554	486	556	447	-2.00	20.39	1.703	2.620	20	26
141	508	337	520	295	-2.20	25.53	1.218	1.860	18	20
162	502	402	502	358	-2.33	21.68	2.658	3.580	22	34
9003	500	294	512	252	-2.24	27.89	5.686	5.700	34	36
171	498	455	500	416	-2.35	20.79	0.029	0.370	6	12
163	488	421	488	377	-2.46	21.29	0.904	1.880	18	20
140	486	333	498	291	-2.37	25.75	0.172	0.290	6	8
173	484	508	486	469	-2.47	19.57	0.413	1.910	18	22
142	484	353	496	311	-2.39	24.64	0.659	0.980	10	18
144	480	379	480	335	-2.53	23.32	0.165	0.240	6	10
114	470	316	482	274	-2.51	26.68	1.003	1.350	18	16
172	464	457	464	413	-2.67	20.83	0.067	0.660	10	14
143	448	363	448	319	-2.81	24.20	0.519	1.220	14	14
138	446	336	458	294	-2.72	25.58	0.427	1.110	12	16
112	426	301	438	259	-2.90	27.51	0.747	1.780	18	18
9004	426	404	426	360	-3.00	21.50	4.198	4.060	30	28
139	416	358	416	314	-3.07	24.48	0.485	1.430	16	16
136	376	352	376	308	-3.31	24.81	0.026	0.160	4	8
158	376	393	376	349	-3.31	22.46	5.207	5.860	30	36
109	374	300	380	253	-3.29	27.84	0.403	1.540	16	18
160	374	428	374	384	-3.33	21.20	0.121	0.770	8	18
135	372	347	372	303	-3.34	25.08	0.012	0.110	2	8
134	330	335	336	288	-3.56	25.91	0.608	1.800	18	18
159	328	427	326	376	-3.62	21.30	0.060	0.720	10	14
137	320	377	318	326	-3.67	23.82	0.582	1.700	18	20
106	318	308	324	261	-3.63	27.40	0.019	0.240	4	10
104	316	303	322	256	-3.65	27.67	0.006	0.080	2	6
133	288	336	294	289	-3.82	25.86	0.707	1.930	20	18
132	260	341	266	294	-3.99	25.58	0.013	0.080	2	6
9005	258	297	264	250	-4.00	28.00	2.975	3.900	26	34
9006	242	397	240	346	-4.21	22.71	9.890	9.940	36	54
131	242	361	240	310	-4.21	24.70	0.486	1.110	10	22

APPENDIX C6-2

Print file name: c.als, Time: 15:20 Date: 12/1/1989 Page:

Filename: c.als
Window = X : 242 ~ 682
Y : 294 ~ 514

Rec#	Spotname	Image	NewX	NewY	II	Area	Ht	Wd
9001	1	c	696	484	1.216	2.860	20	26
120		c	692	253	0.012	0.080	2	6
168		c	692	382	0.131	0.720	12	16
177		c	688	445	0.148	1.010	12	18
166		c	688	356	0.076	0.480	8	12
148		c	686	322	0.360	1.620	16	18
167		c	662	373	0.286	1.170	14	18
176		c	654	440	0.289	1.270	14	18
117		c	648	268	0.713	1.830	16	26
175		c	648	478	0.062	0.420	8	10
145		c	634	304	1.103	2.040	20	20
165		c	624	401	0.462	1.800	18	20
146		c	608	343	0.114	0.850	12	12
116		c	612	259	0.425	1.430	14	20
164		c	584	384	0.402	1.880	18	20
9002	2	c	556	447	1.703	2.620	20	26
141		c	520	295	1.218	1.860	18	20
162		c	502	358	2.658	3.580	22	34
9003	3	c	512	252	5.686	5.700	34	36
171		c	500	416	0.029	0.370	6	12
163		c	488	377	0.904	1.880	18	20
140		c	498	291	0.172	0.290	6	8
173		c	486	469	0.413	1.910	18	22
142		c	496	311	0.659	0.980	10	18
144		c	480	335	0.165	0.240	6	10
114		c	482	274	1.003	1.350	18	16
172		c	464	413	0.067	0.660	10	14
143		c	448	319	0.519	1.220	14	14
138		c	458	294	0.427	1.110	12	16
112		c	438	259	0.747	1.780	18	18
9004	4	c	426	360	4.198	4.060	30	28
139		c	416	314	0.485	1.430	16	16
136		c	376	308	0.026	0.160	4	8
158		c	376	349	5.207	5.860	30	36
109		c	380	253	0.403	1.540	16	18
160		c	374	384	0.121	0.770	8	18
135		c	372	303	0.012	0.110	2	8
134		c	336	288	0.608	1.800	18	18
159		c	326	376	0.060	0.720	10	14
137		c	318	326	0.582	1.700	18	20
106		c	324	261	0.019	0.240	4	10
104		c	322	256	0.006	0.080	2	6
133		c	294	289	0.707	1.930	20	18
132		c	266	294	0.013	0.080	2	6
9005	5	c	264	250	2.975	3.900	26	34
9006	6	c	240	346	9.890	9.940	36	54
131		c	240	310	0.486	1.110	10	22

APPENDIX C6-3

Print file name: c.mks, Time: 15:19 Date: 12/1/1989 Page:

c.mks
Window = X : 242 ~ 682
Y : 294 ~ 514

---------- 6 Markers ----------

Marker_name	X	Y
9001	682	514
9002	554	486
9003	500	294
9004	426	404
9005	258	297
9006	242	397

Print file name: abc.mmh, Time: 17:59 Date: 3/8/1990 Page:

#NS 3 /* # of scans in the match group */
#PI 0.16 /* PI maximum tolerance */
#MW 1.12 /* MW maximum tolerance */
I:C:I:I:R:R:R:R:I:I:I:I

REC	GEL	X	Y	PI	MW	II	AREA	MAT	a	b	c
9001	a	696	484	-1.00	19.00	3.652	5.140	3	9001	9001	9001
218	b	486	521	-2.46	19.71	0.278	1.460	3	155	218	173
166	b	476	326	-2.50	26.56	1.525	1.800	3	102	166	114
113	a	690	319	-1.04	24.20	3.868	5.060	3	113	178	148
137	a	658	369	-1.27	21.38	0.859	1.990	3	137	198	167
112	a	650	274	-1.33	26.68	1.391	1.670	3	112	175	117
157	a	636	457	-1.42	20.02	1.162	2.200	3	157	212	175
110	a	636	308	-1.42	24.80	2.391	3.340	3	110	176	145
149	a	630	402	-1.48	20.96	1.845	2.860	3	149	211	165
207	b	464	470	-2.65	20.72	0.051	0.690	3	145	207	172
135	a	620	348	-1.54	22.54	0.281	1.140	3	135	195	146
107	a	620	268	-1.54	27.01	0.049	0.190	3	107	140	116
167	b	450	342	-2.74	25.69	0.484	1.090	3	103	167	138
148	a	586	389	-1.78	21.12	0.264	1.540	3	148	197	164
9006	c	242	397	-4.21	22.70	9.890	9.940	3	9006	9006	9006
159	c	328	427	-3.61	21.29	0.060	0.720	3	129	187	159
9005	c	258	297	-4.00	28.00	2.975	3.900	3	9005	9005	9005
9002	a	556	447	-2.00	20.38	4.757	5.120	3	9002	9002	9002
106	a	524	302	-2.18	25.13	1.773	2.330	3	106	171	141
9003	a	512	252	-2.24	27.88	8.928	6.710	3	9003	9003	9003
133	a	504	372	-2.31	21.35	3.676	5.800	3	133	193	162
146	a	500	417	-2.34	20.78	0.203	1.300	3	146	208	171
155	a	492	464	-2.42	19.76	0.379	1.910	3	155	218	173
104	a	490	319	-2.44	24.20	1.404	1.380	3	104	168	142
132	a	480	333	-2.52	23.43	0.039	0.080	3	132	191	144
102	a	478	277	-2.54	26.52	1.250	1.540	3	102	166	114
145	a	460	417	-2.70	20.78	0.140	1.140	3	145	207	172
103	a	454	298	-2.75	25.36	0.437	0.980	3	103	167	138
131	a	452	324	-2.77	23.93	1.888	2.170	3	131	169	143
100	a	432	261	-2.95	27.39	0.884	1.910	3	100	134	112
9004	a	426	360	-3.00	21.50	4.162	3.900	3	9004	9004	9004
101	a	416	317	-3.06	24.30	0.131	0.610	3	101	165	139
97	a	380	259	-3.28	27.51	0.702	1.960	3	97	131	109
128	a	376	349	-3.30	22.45	3.781	5.190	3	128	186	158
144	a	372	385	-3.33	21.19	0.051	0.370	3	144	188	160
98	a	366	294	-3.38	25.57	0.026	0.270	3	98	163	135
99	a	334	291	-3.56	25.75	0.162	1.110	3	99	162	134
129	a	332	382	-3.58	21.21	0.074	0.930	3	129	187	159
127	a	324	332	-3.63	23.48	0.191	1.300	3	127	164	137
96	a	322	261	-3.65	27.39	0.150	0.980	3	96	128	106
95	a	292	290	-3.82	25.79	0.296	1.540	3	95	160	133
9005	a	264	250	-4.00	28.00	3.127	4.590	3	9005	9005	9005
191	b	488	392	-2.44	22.87	0.384	0.690	3	132	191	144
9006	a	240	346	-4.21	22.70	7.771	7.790	3	9006	9006	9006
9001	b	714	521	-1.00	19.00	2.609	4.350	3	9001	9001	9001
178	b	712	357	-1.01	24.14	2.703	4.640	3	113	178	148
198	b	668	415	-1.33	21.28	0.514	2.010	3	137	198	167
175	b	656	320	-1.25	26.89	1.309	2.760	3	112	175	117

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186 b	374	393	-3.30	22.82	6.077	5.960	3	128	186	158
160 c	374	428	-3.32	21.20	0.121	0.770	3	144	188	160
176 b	640	351	-1.36	25.19	1.385	2.360	3	110	176	145
158 c	376	393	-3.30	22.45	5.207	5.860	3	128	186	158
211 b	636	454	-1.41	21.02	0.848	2.120	3	149	211	165
162 b	330	327	-3.58	25.46	0.416	1.400	3	99	162	134
195 b	622	392	-1.51	23.27	0.282	1.350	3	135	195	146
140 b	618	310	-1.51	27.45	0.349	1.250	3	107	140	116
187 b	326	421	-3.65	21.17	0.062	0.740	3	129	187	159
197 b	588	434	-1.75	21.28	0.426	1.830	3	148	197	164
164 b	320	369	-3.68	23.37	0.406	1.430	3	127	164	137
133 c	288	336	-3.81	25.86	0.707	1.930	3	95	160	133
128 b	314	296	-3.68	27.18	0.050	0.530	3	96	128	106
9002 b	554	503	-2.00	20.38	2.803	3.290	3	9002	9002	9002
106 c	318	308	-3.63	27.39	0.019	0.240	3	96	128	106
171 b	518	348	-2.18	25.36	2.230	2.460	3	106	171	141
137 c	320	377	-3.67	23.81	0.582	1.700	3	127	164	137
9003 b	506	302	-2.24	27.88	6.837	6.150	3	9003	9003	9003
193 b	504	415	-2.29	21.43	2.542	3.260	3	133	193	162
208 b	500	470	-2.32	20.81	0.075	0.770	3	146	208	171
160 b	288	322	-3.83	25.75	0.489	1.560	3	95	160	133
168 b	490	364	-2.39	24.47	1.919	1.720	3	104	168	142
9001 c	682	514	-1.00	19.00	1.216	2.860	3	9001	9001	9001
139 c	416	358	-3.06	24.47	0.485	1.430	3	101	165	139
112 c	426	301	-2.90	27.51	0.747	1.780	3	100	134	112
138 c	446	336	-2.72	25.57	0.427	1.110	3	103	167	138
143 c	448	363	-2.80	24.20	0.519	1.220	3	131	169	143
134 c	330	335	-3.55	25.90	0.608	1.800	3	99	162	134
169 b	454	369	-2.74	24.14	1.840	2.070	3	131	169	143
135 c	372	347	-3.33	25.07	0.012	0.110	3	98	163	135
114 c	470	316	-2.50	26.68	1.003	1.350	3	102	166	114
109 c	374	300	-3.28	27.84	0.403	1.540	3	97	131	109
134 b	428	303	-2.93	27.84	1.068	1.750	3	100	134	112
9004 b	424	409	-3.00	21.50	2.862	3.070	3	9004	9004	9004
165 b	416	360	-3.04	24.63	0.415	1.400	3	101	165	139
131 b	374	297	-3.30	27.12	0.655	1.670	3	97	131	109
172 c	464	457	-2.67	20.82	0.067	0.660	3	145	207	172
188 b	374	429	-3.30	21.25	0.119	0.720	3	144	188	160
163 b	364	332	-3.38	26.19	0.126	0.820	3	98	163	135
167 c	648	403	-1.25	21.34	0.286	1.170	3	137	198	167
117 c	636	310	-1.35	27.01	0.713	1.830	3	112	175	117
144 c	480	379	-2.52	23.31	0.165	0.240	3	132	191	144
173 c	484	508	-2.47	19.56	0.413	1.910	3	155	218	173
142 c	484	353	-2.39	24.63	0.659	0.980	3	104	168	142
9004 c	426	404	-3.00	21.50	4.198	4.060	3	9004	9004	9004
9003 c	500	294	-2.24	27.88	5.686	5.700	3	9003	9003	9003
162 c	502	402	-2.32	21.68	2.658	3.580	3	133	193	162
9005 b	262	281	-4.00	28.00	4.348	4.350	3	9005	9005	9005
9006 b	244	381	-4.21	22.70	11.183	9.490	3	9006	9006	9006
171 c	498	455	-2.34	20.79	0.029	0.370	3	146	208	171
175 c	634	508	-1.35	19.22	0.062	0.420	3	157	220	175
141 c	508	337	-2.20	25.53	1.218	1.860	3	106	171	141
9002 c	554	486	-2.00	20.38	1.703	2.620	3	9002	9002	9002
164 c	582	423	-1.79	21.20	0.402	1.880	3	148	197	164

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148	c	672	352	-1.08	24.04	0.360	1.620	3	113	178	148
165	c	622	440	-1.51	20.97	0.462	1.800	3	149	211	165
116	c	600	301	-1.60	27.51	0.425	1.430	3	107	140	116
146	c	606	382	-1.62	22.87	0.114	0.850	3	135	195	146
145	c	622	346	-1.45	25.03	1.103	2.040	3	110	176	145
94	a	240	312	-4.21	24.59	0.531	1.190	2	94	0	131
105	a	570	265	-1.89	27.18	0.052	0.720	2	105	137	0
220	b	648	519	-1.48	19.07	0.159	0.900	2	0	220	175
176	c	640	470	-1.29	20.47	0.289	1.270	2	0	213	176
213	b	652	477	-1.45	20.47	0.173	0.870	2	0	213	176
166	c	674	386	-1.05	21.85	0.076	0.480	2	136	0	166
136	a	696	357	-1.00	21.76	0.300	1.030	2	136	0	166
161	b	262	330	-4.00	25.29	0.035	0.190	2	0	161	132
194	b	494	432	-2.39	21.20	0.691	1.720	2	0	194	163
212	b	638	503	-1.54	19.68	0.105	0.580	2	157	212	0
163	c	488	421	-2.46	21.29	0.904	1.880	2	0	194	163
137	b	570	311	-1.86	27.39	0.007	0.130	2	105	137	0
173	b	580	344	-1.78	25.57	0.088	0.770	2	108	173	0
174	b	596	361	-1.67	24.63	0.075	0.560	2	109	174	0
139	b	630	292	-1.42	27.55	0.399	1.190	2	73	139	0
177	c	674	475	-1.05	20.42	0.148	1.010	2	150	0	177
109	a	600	316	-1.69	24.37	0.022	0.190	2	109	174	0
73	a	628	250	-1.49	28.00	1.006	1.800	2	73	139	0
150	a	694	430	-1.01	20.61	1.023	2.620	2	150	0	177
108	a	576	302	-1.86	25.13	0.111	1.090	2	108	173	0
131	c	242	361	-4.21	24.70	0.486	1.110	2	94	0	131
132	c	260	341	-3.99	25.57	0.013	0.080	2	0	161	132
168	c	678	412	-1.02	21.21	0.131	0.720	1	0	0	168
120	c	680	295	-1.02	27.84	0.012	0.080	1	0	0	120
136	c	376	352	-3.30	24.80	0.026	0.160	1	0	0	136
206	b	354	475	-3.44	20.65	0.250	1.510	1	0	206	0
130	b	352	284	-3.45	27.84	0.232	1.190	1	0	130	0
140	c	486	333	-2.36	25.75	0.172	0.290	1	0	0	140
192	b	452	394	-2.75	22.77	0.161	0.370	1	0	192	0
172	b	512	380	-2.21	23.60	0.177	0.500	1	0	172	0
170	b	530	325	-2.10	26.62	0.062	0.290	1	0	170	0
104	c	316	303	-3.65	7.67	0.006	0.080	1	0	0	104
196	b	576	408	-1.85	2.20	0.014	0.210	1	0	196	0
135	b	460	288	-2.65	27.34	0.083	0.560	1	0	135	0
134	a	560	336	-1.99	23.27	0.055	0.480	1	134	0	0
209	b	490	499	-2.42	20.45	0.031	0.400	1	0	209	0
189	b	434	386	-2.92	23.20	0.054	0.160	1	0	189	0

APPENDIX D1-3

Print file name: abc.cls, Time: 11:06 Date: 12/5/1989 Page:

#NS 3 /* # of scans in the match group */
#PI 0.160
#MW 1.120
I:C:I:I:R:R:R:R:I:I:I:I

REC	GEL	X	Y	PI	MW	II	AREA	MAT	a	b	c
157	a	636	457	-1.42	20.02	1.162	2.200	3	157	212	175
175	c	634	508	-1.35	19.22	0.062	0.420	3	157	220	175
220	b	648	519	-1.48	19.07	0.159	0.900	2	0	220	175
212	b	638	503	-1.54	19.68	0.105	0.580	2	157	212	0

APPENDIX D2

Print file name: abc.uni, Time: 11:06 Date: 12/5/1989 Page:

#NS 3 /* # of scans in the match group */
#PI 0.160
#MW 1.120
I:C:I:I:R:R:R:R:I:I:I:I

REC	GEL	X	Y	PI	MW	II	AREA	MAT	a	b	c
168	c	678	412	-1.02	21.21	0.131	0.720	1	0	0	168
120	c	680	295	-1.02	27.84	0.012	0.080	1	0	0	120
136	c	376	352	-3.30	24.80	0.026	0.160	1	0	0	136
206	b	354	475	-3.44	20.65	0.250	1.510	1	0	206	0
130	b	352	284	-3.45	27.84	0.232	1.190	1	0	130	0
140	c	486	333	-2.36	25.75	0.172	0.290	1	0	0	140
192	b	452	394	-2.75	22.77	0.161	0.370	1	0	192	0
172	b	512	380	-2.21	23.60	0.177	0.500	1	0	172	0
170	b	530	325	-2.10	26.62	0.062	0.290	1	0	170	0
104	c	316	303	-3.65	27.67	0.006	0.080	1	0	0	104
196	b	576	408	-1.85	22.20	0.014	0.210	1	0	196	0
135	b	460	288	-2.65	27.34	0.083	0.560	1	0	135	0
134	a	560	336	-1.98	23.27	0.055	0.480	1	134	0	0
209	b	490	499	-2.42	20.45	0.031	0.400	1	0	209	0
189	b	434	386	-2.92	23.20	0.054	0.160	1	0	189	0

APPENDIX D3

Print file name: abc.exm, Time: 11:06 Date: 12/5/1989 Page:

#NS 3 /* # of scans in the match group */
#PI 0.160
#MW 1.120
I:C:I:I:R:R:R:R:I:I:I:I

REC	GEL	X	Y	PI	MW	II	AREA	MAT	a	b	c
177	c	674	475	-1.05	20.42	0.148	1.010	2	150	0	177
150	a	694	430	-1.01	20.61	1.023	2.620	2	150	0	177
139	b	630	292	-1.42	27.55	0.399	1.190	2	73	139	0
73	a	628	250	-1.49	28.00	1.006	1.800	2	73	139	0
174	b	596	361	-1.67	24.63	0.075	0.560	2	109	174	0
109	a	600	316	-1.69	24.37	0.022	0.190	2	109	174	0
173	b	580	344	-1.78	25.57	0.088	0.770	2	108	173	0
108	a	576	302	-1.86	25.13	0.111	1.090	2	108	173	0
194	b	494	432	-2.39	21.20	0.691	1.720	2	0	194	163
163	c	488	421	-2.46	21.29	0.904	1.880	2	0	194	163
161	b	262	330	-4.00	25.29	0.035	0.190	2	0	161	132
132	c	260	341	-3.99	25.57	0.013	0.080	2	0	161	132
166	c	674	386	-1.05	21.85	0.076	0.480	2	136	0	166
136	a	696	357	-1.00	21.76	0.300	1.030	2	136	0	166
176	c	640	470	-1.29	20.47	0.289	1.270	2	0	213	176
213	b	652	477	-1.45	20.47	0.173	0.870	2	0	213	176
105	a	570	265	-1.89	27.18	0.052	0.720	2	105	137	0
137	b	570	311	-1.86	27.39	0.007	0.130	2	105	137	0
94	a	240	312	-4.21	24.59	0.531	1.190	2	94	0	131
131	c	242	361	-4.21	24.70	0.486	1.110	2	94	0	131
95	a	292	290	-3.82	25.79	0.296	1.540	3	95	160	133
133	c	288	336	-3.81	25.86	0.707	1.930	3	95	160	133
160	b	288	322	-3.83	25.75	0.489	1.560	3	95	160	133
96	a	322	261	-3.65	27.39	0.150	0.980	3	96	128	106
128	b	314	296	-3.68	27.18	0.050	0.530	3	96	128	106
106	c	318	308	-3.63	27.39	0.019	0.240	3	96	128	106
127	a	324	332	-3.63	23.48	0.191	1.300	3	127	164	137
164	b	320	369	-3.68	23.37	0.406	1.430	3	127	164	137
137	c	320	377	-3.67	23.81	0.582	1.700	3	127	164	137
99	a	334	291	-3.56	25.75	0.162	1.110	3	99	162	134
162	b	330	327	-3.58	25.46	0.416	1.400	3	99	162	134
134	c	330	335	-3.55	25.90	0.608	1.800	3	99	162	134
98	a	366	294	-3.38	25.57	0.026	0.270	3	98	163	135
135	c	372	347	-3.33	25.07	0.012	0.110	3	98	163	135
163	b	364	332	-3.38	26.19	0.126	0.820	3	98	163	135
144	a	372	385	-3.33	21.19	0.051	0.370	3	144	188	160
160	c	374	428	-3.32	21.20	0.121	0.770	3	144	188	160
188	b	374	429	-3.30	21.25	0.119	0.720	3	144	188	160
128	a	376	349	-3.30	22.45	3.781	5.190	3	128	186	158
186	b	374	393	-3.30	22.82	6.077	5.960	3	128	186	158
158	c	376	393	-3.30	22.45	5.207	5.860	3	128	186	158
97	a	380	259	-3.28	27.51	0.702	1.960	3	97	131	109
109	c	374	300	-3.28	27.84	0.403	1.540	3	97	131	109
131	b	374	297	-3.30	27.12	0.655	1.670	3	97	131	109
101	a	416	317	-3.06	24.30	0.131	0.610	3	101	165	139
139	c	416	358	-3.06	24.47	0.485	1.430	3	101	165	139
165	b	416	360	-3.04	24.63	0.415	1.400	3	101	165	139
9004	a	426	360	-3.00	21.50	4.162	3.900	3	9004	9004	9004

Print file name: abc.exm, Time: 11:06 Date: 12/5/1989 Page:

9004 b	424	409	-3.00	21.50	2.862	3.070	3	9004	9004	9004
9004 c	426	404	-3.00	21.50	4.198	4.060	3	9004	9004	9004
100 a	432	261	-2.95	27.39	0.884	1.910	3	100	134	112
112 c	426	301	-2.90	27.51	0.747	1.780	3	100	134	112
134 b	428	303	-2.93	27.84	1.068	1.750	3	100	134	112
131 a	452	324	-2.77	23.93	1.888	2.170	3	131	169	143
143 c	448	363	-2.80	24.20	0.519	1.220	3	131	169	143
169 b	454	369	-2.74	24.14	1.840	2.070	3	131	169	143
132 a	480	333	-2.52	23.43	0.039	0.080	3	132	191	144
191 b	488	392	-2.44	22.87	0.384	0.690	3	132	191	144
144 c	480	379	-2.52	23.31	0.165	0.240	3	132	191	144
104 a	490	319	-2.44	24.20	1.404	1.380	3	104	168	142
168 b	490	364	-2.39	24.47	1.919	1.720	3	104	168	142
142 c	484	353	-2.39	24.63	0.659	0.980	3	104	168	142
146 a	500	417	-2.34	20.78	0.203	1.300	3	146	208	171
208 b	500	470	-2.32	20.81	0.075	0.770	3	146	208	171
171 c	498	455	-2.34	20.79	0.029	0.370	3	146	208	171
133 a	504	372	-2.31	21.35	3.676	5.800	3	133	193	162
193 b	504	415	-2.29	21.43	2.542	3.260	3	133	193	162
162 c	502	402	-2.32	21.68	2.658	3.580	3	133	193	162
9003 a	512	252	-2.24	27.88	8.928	6.710	3	9003	9003	9003
9003 b	506	302	-2.24	27.88	6.837	6.150	3	9003	9003	9003
9003 c	500	294	-2.24	27.88	5.686	5.700	3	9003	9003	9003
106 a	524	302	-2.18	25.13	1.773	2.330	3	106	171	141
171 b	518	348	-2.18	25.36	2.230	2.460	3	106	171	141
141 c	508	337	-2.20	25.53	1.218	1.860	3	106	171	141
9002 a	556	447	-2.00	20.38	4.757	5.120	3	9002	9002	9002
9002 b	554	503	-2.00	20.38	2.803	3.290	3	9002	9002	9002
9002 c	554	486	-2.00	20.38	1.703	2.620	3	9002	9002	9002
9005 c	258	297	-4.00	28.00	2.975	3.900	3	9005	9005	9005
9005 a	264	250	-4.00	28.00	3.127	4.590	3	9005	9005	9005
9005 b	262	281	-4.00	28.00	4.348	4.350	3	9005	9005	9005
159 c	328	427	-3.61	21.29	0.060	0.720	3	129	187	159
129 a	332	382	-3.58	21.21	0.074	0.930	3	129	187	159
187 b	326	421	-3.65	21.17	0.062	0.740	3	129	187	159
9006 c	242	397	-4.21	22.70	9.890	9.940	3	9006	9006	9006
9006 a	240	346	-4.21	22.70	7.771	7.790	3	9006	9006	9006
9006 b	244	381	-4.21	22.70	11.183	9.490	3	9006	9006	9006
148 a	586	389	-1.78	21.12	0.264	1.540	3	148	197	164
197 b	588	434	-1.75	21.28	0.426	1.830	3	148	197	164
164 c	582	423	-1.79	21.20	0.402	1.880	3	148	197	164
167 b	450	342	-2.74	25.69	0.484	1.090	3	103	167	138
103 a	454	298	-2.75	25.36	0.437	0.980	3	103	167	138
138 c	446	336	-2.72	25.57	0.427	1.110	3	103	167	138
107 a	620	268	-1.54	27.01	0.049	0.190	3	107	140	116
140 b	618	310	-1.51	27.45	0.349	1.250	3	107	140	116
116 c	600	301	-1.60	27.51	0.425	1.430	3	107	140	116
135 a	620	348	-1.54	22.54	0.281	1.140	3	135	195	146
195 b	622	392	-1.51	23.27	0.282	1.350	3	135	195	146
146 c	606	382	-1.62	22.87	0.114	0.850	3	135	195	146
207 b	464	470	-2.65	20.72	0.051	0.690	3	145	207	172
145 a	460	417	-2.70	20.78	0.140	1.140	3	145	207	172
172 c	464	457	-2.67	20.82	0.067	0.660	3	145	207	172
149 a	630	402	-1.48	20.96	1.845	2.860	3	149	211	165

APPENDIX D4-2

Print file name: abc.exm, Time: 11:06 Date: 12/5/1989 Page:

211	b	636	454	-1.41	21.02	0.848	2.120	3	149	211	165
165	c	622	440	-1.51	20.97	0.462	1.800	3	149	211	165
110	a	636	308	-1.42	24.80	2.391	3.340	3	110	176	145
176	b	640	351	-1.36	25.19	1.385	2.360	3	110	176	145
145	c	622	346	-1.45	25.03	1.103	2.040	3	110	176	145
112	a	650	274	-1.33	26.68	1.391	1.670	3	112	175	117
175	b	656	320	-1.25	26.89	1.309	2.760	3	112	175	117
117	c	636	310	-1.35	27.01	0.713	1.830	3	112	175	117
137	a	658	369	-1.27	21.38	0.859	1.990	3	137	198	167
198	b	668	415	-1.33	21.28	0.514	2.010	3	137	198	167
167	c	648	403	-1.25	21.34	0.286	1.170	3	137	198	167
113	a	690	319	-1.04	24.20	3.868	5.060	3	113	178	148
178	b	712	357	-1.01	24.14	2.703	4.640	3	113	178	148
148	c	672	352	-1.08	24.04	0.360	1.620	3	113	178	148
166	b	476	326	-2.50	26.56	1.525	1.800	3	102	166	114
102	a	478	277	-2.54	26.52	1.250	1.540	3	102	166	114
114	c	470	316	-2.50	26.68	1.003	1.350	3	102	166	114
218	b	486	521	-2.46	19.71	0.278	1.460	3	155	218	173
155	a	492	464	-2.42	19.76	0.379	1.910	3	155	218	173
173	c	484	508	-2.47	19.56	0.413	1.910	3	155	218	173
9001	a	696	484	-1.00	19.00	3.652	5.140	3	9001	9001	9001
9001	b	714	521	-1.00	19.00	2.609	4.350	3	9001	9001	9001
9001	c	682	514	-1.00	19.00	1.216	2.860	3	9001	9001	9001

Print file name: abc.cmp. Time: 11:05 Date: 12/5/1989 Page:

#NS 3 /* # of scans in the match group */
#PI 0.160
#MW 1.120
I:C:I:I:R:R:R:R:I:I:I:I

REC	GEL	X	Y	PI	MW	II	AREA	MAT	a	b	c
-10	abc	-1	-1	-4.21	24.65	0.508	1.150	2	94	0	131
-6	abc	-1	-1	-3.99	25.43	0.024	0.135	2	0	161	132
-11	abc	-1	-1	-3.82	25.80	0.497	1.677	3	95	160	133
-13	abc	-1	-1	-3.66	23.55	0.393	1.477	3	127	164	137
104	c	316	303	-3.65	27.67	0.006	0.080	1	0	0	104
-12	abc	-1	-1	-3.65	27.32	0.073	0.583	3	96	128	106
-31	abc	-1	-1	-3.61	21.22	0.065	0.797	3	129	187	159
-14	abc	-1	-1	-3.56	25.70	0.395	1.437	3	99	162	134
130	b	352	284	-3.45	27.84	0.232	1.190	1	0	130	0
206	b	354	475	-3.44	20.65	0.250	1.510	1	0	206	0
-15	abc	-1	-1	-3.36	25.61	0.055	0.400	3	98	163	135
-16	abc	-1	-1	-3.32	21.21	0.097	0.620	3	144	188	160
136	c	376	352	-3.30	24.80	0.026	0.160	1	0	0	136
-17	abc	-1	-1	-3.30	22.57	5.022	5.670	3	128	186	158
-18	abc	-1	-1	-3.29	27.49	0.587	1.723	3	97	131	109
-19	abc	-1	-1	-3.05	24.47	0.344	1.147	3	101	165	139
-21	abc	-1	-1	-2.93	27.58	0.900	1.813	3	100	134	112
189	b	434	386	-2.92	23.20	0.054	0.160	1	0	189	0
-22	abc	-1	-1	-2.77	24.09	1.416	1.820	3	131	169	143
192	b	452	394	-2.75	22.77	0.161	0.370	1	0	192	0
-34	abc	-1	-1	-2.74	25.54	0.449	1.060	3	103	167	138
-37	abc	-1	-1	-2.67	20.77	0.086	0.830	3	145	207	172
135	b	460	288	-2.65	27.34	0.083	0.560	1	0	135	0
-45	abc	-1	-1	-2.51	26.59	1.259	1.563	3	102	166	114
-23	abc	-1	-1	-2.49	23.20	0.196	0.337	3	132	191	144
-46	abc	-1	-1	-2.45	19.68	0.357	1.760	3	155	218	173
-5	abc	-1	-1	-2.43	21.25	0.798	1.800	2	0	194	163
209	b	490	499	-2.42	20.45	0.031	0.400	1	0	209	0
-24	abc	-1	-1	-2.41	24.43	1.327	1.360	3	104	168	142
140	c	486	333	-2.36	25.75	0.172	0.290	1	0	0	140
-25	abc	-1	-1	-2.33	20.79	0.102	0.813	3	146	208	171
-26	abc	-1	-1	-2.31	21.49	2.959	4.213	3	133	193	162
172	b	512	380	-2.21	23.60	0.177	0.500	1	0	172	0
-28	abc	-1	-1	-2.19	25.34	1.740	2.217	3	106	171	141
170	b	530	325	-2.10	26.62	0.062	0.290	1	0	170	0
134	a	560	336	-1.98	23.27	0.055	0.480	1	134	0	0
-9	abc	-1	-1	-1.88	27.28	0.030	0.425	2	105	137	0
196	b	576	408	-1.85	22.20	0.014	0.210	1	0	196	0
-4	abc	-1	-1	-1.82	25.35	0.100	0.930	2	108	173	0
-33	abc	-1	-1	-1.77	21.20	0.364	1.750	3	148	197	164
-3	abc	-1	-1	-1.68	24.50	0.049	0.375	2	109	174	0
-36	abc	-1	-1	-1.56	22.89	0.226	1.113	3	135	195	146
-35	abc	-1	-1	-1.55	27.32	0.274	0.957	3	107	140	116
-40	abc	0	0	-1.48	19.85	0.633	1.390	2	157	212	0
-38	abc	-1	-1	-1.47	20.98	1.052	2.260	3	149	211	165
-2	abc	-1	-1	-1.45	27.77	0.702	1.495	2	73	139	0
-39	abc	-1	-1	-1.41	25.01	1.626	2.580	3	110	176	145
-41	abc	0	0	-1.41	19.15	0.110	0.660	2	0	220	175

Print file name: abc.cmp, Time: 11:05 Date: 12/5/1989 Page:

-8	abc	-1	-1	-1.37	20.47	0.231	1.070	2	0	213	176
-42	abc	-1	-1	-1.31	26.86	1.138	2.087	3	112	175	117
-43	abc	-1	-1	-1.28	21.33	0.553	1.723	3	137	198	167
-44	abc	-1	-1	-1.04	24.13	2.310	3.773	3	113	178	148
-1	abc	-1	-1	-1.03	20.51	0.586	1.815	2	150	0	177
168	c	678	412	-1.02	21.21	0.131	0.720	1	0	0	168
120	c	680	295	-1.02	27.84	0.012	0.080	1	0	0	120
-7	abc	-1	-1	-1.02	21.81	0.188	0.755	2	136	0	166
-32	abc	-1	-1	-4.21	22.70	9.615	9.073	3	9006	9006	9006
-30	abc	-1	-1	-4.00	28.00	3.483	4.280	3	9005	9005	9005
-20	abc	-1	-1	-3.00	21.50	3.741	3.677	3	9004	9004	9004
-27	abc	-1	-1	-2.24	27.88	7.150	6.187	3	9003	9003	9003
-29	abc	-1	-1	-2.00	20.38	3.088	3.677	3	9002	9002	9002
-47	abc	-1	-1	-1.00	19.00	2.492	4.117	3	9001	9001	9001

Print file name: abc.smh, Time: 17:33 Date: 3/6/1990 Page: 1

```
#NS 3  /* abc.smh       3/6/1990 */
#PI 0.12
#MW 0.80
i:c:i:i:r:r:r:r:i:i:i:i:
```

REC	GEL	X	Y	PI	MW	II	AREA	MAT	a	b	c
94	a	240	312	-4.210	24.590	0.531	1.190	2	94	0	131
9006	a	240	346	-4.210	22.700	7.771	7.790	3	9006	9006	9006
9005	a	264	250	-4.000	28.000	3.127	4.590	3	9005	9005	9005
95	a	292	290	-3.820	25.790	0.296	1.540	3	95	160	133
96	a	322	261	-3.650	27.390	0.150	0.980	3	96	128	106
127	a	324	332	-3.630	23.480	0.191	1.300	3	127	164	137
129	a	332	382	-3.580	21.210	0.074	0.930	3	129	187	159
99	a	334	291	-3.560	25.750	0.162	1.110	3	99	162	134
98	a	366	294	-3.380	25.570	0.026	0.270	3	98	163	135
144	a	372	385	-3.330	21.190	0.051	0.370	3	144	188	160
128	a	376	349	-3.300	22.450	3.781	5.190	3	128	186	158
97	a	380	259	-3.280	27.510	0.702	1.960	3	97	131	109
101	a	416	317	-3.060	24.300	0.131	0.610	3	101	165	139
9004	a	426	360	-3.000	21.500	4.162	3.900	3	9004	9004	9004
100	a	432	261	-2.950	27.390	0.884	1.910	3	100	134	112
131	a	452	324	-2.770	23.930	1.888	2.170	3	131	169	143
103	a	454	298	-2.750	25.360	0.437	0.980	3	103	167	138
145	a	460	417	-2.700	20.780	0.140	1.140	3	145	207	172
102	a	478	277	-2.540	26.520	1.250	1.540	3	102	166	114
132	a	480	333	-2.520	23.430	0.039	0.080	3	132	191	144
104	a	490	319	-2.440	24.200	1.404	1.380	3	104	168	142
155	a	492	464	-2.420	19.760	0.379	1.910	3	155	218	173
146	a	500	417	-2.340	20.780	0.203	1.300	3	146	208	171
133	a	504	372	-2.310	21.350	3.676	5.800	3	133	193	162
9003	a	512	252	-2.240	27.880	8.928	6.710	3	9003	9003	9003
106	a	524	302	-2.180	25.130	1.773	2.330	3	106	171	141
9002	a	556	447	-2.000	20.380	4.757	5.120	3	9002	9002	9002
134	a	560	336	-1.980	23.270	0.055	0.480	1	134	0	0
105	a	570	265	-1.890	27.180	0.052	0.720	2	105	137	0
108	a	576	302	-1.860	25.130	0.111	1.090	2	108	173	0
148	a	586	389	-1.780	21.120	0.264	1.540	3	148	197	164
109	a	600	316	-1.690	24.370	0.022	0.190	2	109	174	0
107	a	620	268	-1.540	27.010	0.049	0.190	3	107	140	116
135	a	620	348	-1.540	22.540	0.281	1.140	3	135	195	146
73	a	628	250	-1.490	28.000	1.006	1.800	2	73	139	0
149	a	630	402	-1.480	20.960	1.845	2.860	3	149	211	165
110	a	636	308	-1.420	24.800	2.391	3.340	3	110	176	145
157	a	636	457	-1.420	20.020	1.162	2.200	3	157	212	175
112	a	650	274	-1.330	26.680	1.391	1.670	3	112	175	117
137	a	658	369	-1.270	21.380	0.859	1.990	3	137	198	167
113	a	690	319	-1.040	24.200	3.868	5.060	3	113	178	148
150	a	694	430	-1.010	20.610	1.023	2.620	2	150	0	177
9001	a	696	484	-1.000	19.000	3.652	5.140	3	9001	9001	9001
136	a	696	357	-1.000	21.760	0.300	1.030	2	136	0	166

APPENDIX E1

Print file name: abc.pmm, Time: 17:32 Date: 3/6/1990 Page: 1

```
#NS 3  /* abc.pmm       3/6/1990 */
#PI 0.12
#MW 0.80
i:c:i:i:r:r:r:r:i:i:i:i:
  REC   GEL     X     Y       PI       MW       II     AREA  MAT     a     b     c
  157     a   636   457   -1.420   20.020    1.162    2.200    3   157   212   175
```

APPENDIX E2

Print file name: abc.pcm, Time: 17:32 Date: 3/6/1990 Page: 1

```
#NS 3  /* abc.pcm       3/6/1990 */
#PI 0.12
#MW 0.80
i:c:i:i:r:r:r:r:i:i:i:i:
```

REC	GEL	X	Y	PI	MW	II	AREA	MAT	a	b	c
94	a	240	312	-4.210	24.590	0.531	1.190	2	94	0	131
9006	a	240	346	-4.210	22.700	7.771	7.790	3	9006	9006	9006
9005	a	264	250	-4.000	28.000	3.127	4.590	3	9005	9005	9005
95	a	292	290	-3.820	25.790	0.296	1.540	3	95	160	133
96	a	322	261	-3.650	27.390	0.150	0.980	3	96	128	106
127	a	324	332	-3.630	23.480	0.191	1.300	3	127	164	137
129	a	332	382	-3.580	21.210	0.074	0.930	3	129	187	159
99	a	334	291	-3.560	25.750	0.162	1.110	3	99	162	134
98	a	366	294	-3.380	25.570	0.026	0.270	3	98	163	135
144	a	372	385	-3.330	21.190	0.051	0.370	3	144	188	160
128	a	376	349	-3.300	22.450	3.781	5.190	3	128	186	158
97	a	380	259	-3.280	27.510	0.702	1.960	3	97	131	109
101	a	416	317	-3.060	24.300	0.131	0.610	3	101	165	139
9004	a	426	360	-3.000	21.500	4.162	3.900	3	9004	9004	9004
100	a	432	261	-2.950	27.390	0.884	1.910	3	100	134	112
131	a	452	324	-2.770	23.930	1.888	2.170	3	131	169	143
103	a	454	298	-2.750	25.360	0.437	0.980	3	103	167	138
145	a	460	417	-2.700	20.780	0.140	1.140	3	145	207	172
102	a	478	277	-2.540	26.520	1.250	1.540	3	102	166	114
132	a	480	333	-2.520	23.430	0.039	0.080	3	132	191	144
104	a	490	319	-2.440	24.200	1.404	1.380	3	104	168	142
155	a	492	464	-2.420	19.760	0.379	1.910	3	155	218	173
146	a	500	417	-2.340	20.780	0.203	1.300	3	146	208	171
133	a	504	372	-2.310	21.350	3.676	5.800	3	133	193	162
9003	a	512	252	-2.240	27.880	8.928	6.710	3	9003	9003	9003
106	a	524	302	-2.180	25.130	1.773	2.330	3	106	171	141
9002	a	556	447	-2.000	20.380	4.757	5.120	3	9002	9002	9002
134	a	560	336	-1.980	23.270	0.055	0.480	1	134	0	0
105	a	570	265	-1.890	27.180	0.052	0.720	2	105	137	0
108	a	576	302	-1.860	25.130	0.111	1.090	2	108	173	0
148	a	586	389	-1.780	21.120	0.264	1.540	3	148	197	164
109	a	600	316	-1.690	24.370	0.022	0.190	2	109	174	0
107	a	620	268	-1.540	27.010	0.049	0.190	3	107	140	116
135	a	620	348	-1.540	22.540	0.281	1.140	3	135	195	146
73	a	628	250	-1.490	28.000	1.006	1.800	2	73	139	0
149	a	630	402	-1.480	20.960	1.845	2.860	3	149	211	165
110	a	636	308	-1.420	24.800	2.391	3.340	3	110	176	145
112	a	650	274	-1.330	26.680	1.391	1.670	3	112	175	117
137	a	658	369	-1.270	21.380	0.859	1.990	3	137	198	167
113	a	690	319	-1.040	24.200	3.868	5.060	3	113	178	148
150	a	694	430	-1.010	20.610	1.023	2.620	2	150	0	177
9001	a	696	484	-1.000	19.000	3.652	5.140	3	9001	9001	9001
136	a	696	357	-1.000	21.760	0.300	1.030	2	136	0	166

APPENDIX E3

We Claim:

1. A method of matching two-dimensional (2-D) patterns, said method comprising the steps of:

(a) image scanning a plurality of 2-D patterns and producing corresponding data files for each scanned 2-D pattern and recording logistic data and pattern physical characteristics data in a scan coordinate system;

(b) identifying pattern members in each of said scanned 2-D pattern that bound investigative patterns and designating said identified pattern members as marker members;

(c) designating one of said plurality of 2-D pattern as a reference 2-D pattern, said reference 2-D pattern having a reference pattern member data file which includes a set of reference marker members and unknown reference pattern members each having respective coordinates in said scan coordinate system;

(d) designating at least one of remaining ones of said plurality of 2-D patterns as a study 2-D pattern, said study 2-D pattern having a study pattern data file which includes a set of study marker members and unknown study pattern members each having respective coordinates in said scan coordinate system;

(e) performing a first transformation step that transforms positional coordinates of said set of reference marker members, said unknown reference pattern members and each member of said set of study marker pattern members, from said scan coordinate system to a reference coordinate system, said first transformation step resulting in each member of said set of study marker members being in a registered relationship with a corresponding member of said set of reference marker members;

(f) performing a second transformation step that transforms positional coordinates of each of said unknown study pattern members from said scan coordinate system to

said reference coordinate system and generating at least one adjusted data file containing new coordinate information for all pattern members manipulated by said first and second transformation steps;

(g) repeating said steps (d), (e) and (f) on any remaining one of said plurality of 2-D pattern; and

(h) comparing coordinates of all pattern members in said at least one adjusted data file and producing results identifying matching pattern members.

2. A method of matching two-dimensional (2-D) patterns, as recited in claim 1, wherein said step (h) further includes the steps of:

verifying that potentially matching unknown spots are within an acceptable vector area formed by marker spot vectors before producing said matching results; and

resolving matching results having contradictory matching information among spot pattern members.

3. A method of matching two-dimensional (2-D) patterns, as recited in claim 1, wherein:

said 2-D patterns being protein spot patterns in a plurality of two-dimensional gel electrophoretograms (2-D gels) and said step of identifying said pattern members as marker members further includes assigning isoelectric focusing (PI), and molecular weight (MW) dimensional separation values to said marker members; and

said method further includes after performing said second transformation step, interpolating said assigned PI and MW separation values to said marker members to determine PI and MW values for said unknown study patterns.

4. A method of matching two-dimensional (2-D) patterns, as recited in claim 3, wherein:

said step of comparing includes the step of verifying that potentially matching unknown spots are within an acceptable vector area formed by marker spot vectors before producing said matching results;

said method further includes the step of analyzing said matching results using PI and MW separation values resulting from said interpolating step; and

resolving matching results having contradictory matching information among pattern members.

5. A method of matching two-dimensional (2-D) patterns, as recited in claim 3, wherein after said step of comparing and producing matching results includes:

analyzing said matching results using PI and MW separation values resulting from said interpolating step; and

repeating said steps (b) through (h) and said analyzing step.

6. A method of matching protein spot patterns in a plurality of two-dimensional gel electrophoretograms (2-D gels), said method comprising the steps of:

(a) image scanning each of said plurality of 2-D gels and producing corresponding spot data files for each 2-D gel that contain logistic data and spot physical characteristics data in a scan coordinate system;

(b) identifying spot members in each of said plurality of 2-D gels that bound investigative spot patterns and designating said identified spot members as marker spot members;

(c) designating one of said plurality of 2-D gels as a reference 2-D gel, said reference 2-D gel having an associated reference spot data file including a set of

reference marker spot members and unknown reference spot members having respective coordinates in said scan coordinate system;

(d) designating at least one of remaining ones of said plurality of 2-D gels as a study 2-D gel, said study 2-D gel having an associated study spot data file including a set of study marker spot members and unknown study spot members having respective coordinates in said scan coordinate system;

(e) performing a first transformation step that transforms positional coordinates of said set of reference marker spot members, said unknown reference spot members and each member of said set of study marker spot members from said scan coordinate system to a reference coordinate system, said first transformation step resulting in each member of said set of study marker spot members being in a registered relationship with a corresponding member of said set of reference marker spot members;

(f) performing a second transformation step that transforms positional coordinates of each of said unknown study spot members from said scan coordinate system to said reference coordinate system and generating at least one adjusted data file containing new coordinate information for all spot pattern members manipulated by said first and second transformation steps;

(g) repeating said steps (d), (e) and (f) on any remaining one of said plurality of 2-D gels; and

(h) comparing coordinates of all spot pattern members in said at least one adjusted data file and producing results identifying matching spot pattern members.

7. A method of matching protein spot patterns in a plurality of two-dimensional gel electrophoretograms, as recited in claim 6, wherein said step of performing a second transformation step comprises:

(i) determining an effective range associated with each study marker spot member of said set of study marker spot members,

(ii) determining an attraction pairing relationship between a particular study marker spot member and a particular unknown study spot member, said attraction pairing relationship being determined utilizing said effective range as determined for said particular study marker spot member,

(iii) determining positional coordinates in said reference coordinate system of said particular unknown study spot member by adjusting original scan coordinates by shift amounts equivalent to transformation shift amounts of said particular study marker spot member that resulted from said first transformation step, and

(iv) repeating said (ii) and (iii) steps for all unknown study spot members.

8. A method of matching protein spot patterns in a plurality of two-dimensional gel electrophoretograms, as recited in claim 6, wherein:

said step of identifying said spot members as marker spot members further includes assigning isoelectric focusing (PI), and molecular weight (MW) dimensional separation values to said marker spot members; and

said method further including, after performing said second transformation step, interpolating said assigned PI and MW separation values to said marker spot members to determine PI and MW values for said unknown study patterns.

9. A method of matching protein spot patterns in a plurality of two-dimensional gel electrophoretograms, as recited in claim 8, wherein:

said step of comparing includes the step of verifying that potentially matching unknown spots are within an

acceptable vector area formed by marker spot vectors before producing said matching results; and

said producing matching results includes generating a matched and unmatched spot datafiles for said unknown study spot members.

10. A method of matching protein spot patterns in a plurality of two-dimensional gel electrophoretograms, as recited in claim 9, wherein:

said producing matching results further includes generating a cluster datafile having contradictory matching information about certain ones of said unknown study spot members that match certain other ones of said unknown spot members in a contradictory manner; and

said method further includes resolving said contradictory matching information, producing spot matching results void of said contradictory matching information and updating matching results as required to improve accuracy and efficiency of the matching task.

11. A method of matching protein spot patterns in a plurality of two-dimensional gel electrophoretograms, as recited in claim 10, wherein:

said unmatched spot datafile comprises a unique datafile having said unknown study spot members with coordinates that do not match with any other spot members.

12. A method of matching protein spot patterns in a plurality of two-dimensional gel electrophoretograms, as recited in claim 10, wherein:

said verification step includes a juxtaposition comparison that involves moving a constructed unknown spot's vector formed from a pair of said potentially matching unknown spots towards a pair of marker spot's vectors such that their tails have a common point for determining whether

said unknown spot's vector is within said acceptable area formed by said pair of marker spot's vectors to verify that said potentially matching unknown spots indeed match; and

said matched spot datafile comprises an exact match spot datafile for spot members having been manipulated by said verification step.

13. A method of matching protein spot patterns in a plurality of two-dimensional gel electrophoretograms, as recited in claim 10, wherein:

said matched spots datafile comprises a composite datafile for producing a pseudo spot pattern representing the matched and unmatched spots.

14. A method of matching protein spot patterns in a plurality of two-dimensional gel electrophoretograms, as recited in claim 9, wherein said producing matching results further includes:

generating a single reference gel based matching spot datafile;

generating in background a multiple reference gel based matching spot datafile having contradictory spot matching data and resolving said contradiction and producing a composite matching spot datafile; and

comparing said single reference gel based matching spot datafile with said composite matching spot datafile and further generating a potential mis-matched spot members datafile and a potential matched spot members datafile for improving accuracy of said spot matching results.

15. A method of matching protein spot patterns in a plurality of two-dimensional gel electrophoretograms, as recited in claim 6, wherein:

said logistic data and said spot physical characteristics data in said scan coordinate system

comprises:
gel record number, spot name, image (gel) name, x coordinates, y coordinates, integrated intensity and area.

16. A method of matching protein spot patterns in a plurality of two-dimensional gel electrophoretograms (2-D gels), said method comprising the steps of:

(a) image scanning each of said plurality of 2-D gels and producing corresponding spot data files for each 2-D gel that contain logistic data and spot physical characteristics data in a scan coordinate system;

(b) identifying spot members in each of said plurality of 2-D gels that bound investigative spot patterns and designating said identified spot members as marker spot members;

(c) designating one of said plurality of 2-D gels as a reference 2-D gel, said reference 2-D gel having an associated reference spot data file including a set of reference marker spot members and unknown reference spot members having respective coordinates in said scan coordinate system;

(d) designating at least one of remaining ones of said plurality of 2-D gels as a study 2-D gel, said study 2-D gel having an associated study spot data file including a set of study marker spot members and unknown study spot members having respective coordinates in said scan coordinate system;

(e) performing a first transformation step that transforms positional coordinates of said set of reference marker spot members, said unknown reference spot members and each member of said set of study marker spot members from said scan coordinate system to a reference coordinate system, said first transformation step resulting in each member of said set of study marker spot members being in a registered relationship with a corresponding member of said

set of reference marker spot members;

(f) performing a second transformation step that transforms positional coordinates of each of said unknown study spot members from said scan coordinate system to said reference coordinate system, said second transformation comprising:

(i) determining an effective range associated with each study marker spot member of said set of study marker spot members,

(ii) determining an attraction pairing relationship between a particular study marker spot member and a particular unknown study spot member, said attraction pairing relationship being determined utilizing said effective range as determined for said particular study marker spot member,

(iii) determining positional coordinates in said reference coordinate system of said particular unknown study spot member by adjusting original scan coordinates by shift amounts equivalent to transformation shift amounts of said particular study marker spot member that resulted from said first transformation step, and inputting said determined positional coordinates into at least one adjusted data file containing new coordinate information for all spot pattern members manipulated by said first and second transformation steps;

(iv) repeating said (ii) and (iii) steps for all unknown study spot members;

(g) repeating said steps (d), (e) and (f) on any remaining one of said plurality of 2-D gels; and

(h) comparing coordinates of all spot pattern members in said at least one adjusted data file and producing results identifying matching spot pattern members.

17. A method of matching protein spot patterns in a plurality of two-dimensional gel electrophoretograms, as recited in claim 16, wherein:

said step of comparing includes the step of verifying that potentially matching unknown spots are within an acceptable vector area formed by marker spot vectors before producing said matching results;

said producing matching results includes generating a matched and unmatched spot datafiles for said unknown study spot members;

said method further includes generating a cluster datafile having contradictory matching information about certain ones of said unknown study spot members that match certain other ones of said unknown spot members in a contradictory manner; and

resolving said contradictory matching information and producing spot matching results void of said contradictory matching information.

18. A method of matching protein spot patterns in a plurality of two-dimensional gel electrophoretograms, as recited in claim 17, wherein:

said unmatched spot datafile comprises a unique datafile having said unknown study spot members with coordinates that do not match with any other spot members.

19. A method of matching protein spot patterns in a plurality of two-dimensional gel electrophoretograms, as recited in claim 17, wherein:

said verification step includes a juxtaposition comparison that involves moving a constructed unknown spot's vector formed from a pair of said potentially matching unknown spots towards a pair of marker spot's vectors such that their tails have a common point for determining whether said unknown spot's vector is within said acceptable area

formed by said pair of marker spot's vectors to verify that said potentially matching unknown spots indeed match; and

said matched spot datafile comprises an exact match spot datafile for spot members having been manipulated by said verification step.

20. A method of matching protein spot patterns in a plurality of two-dimensional gel electrophoretograms, as recited in claim 17, wherein:

said matched spots datafile comprises a composite datafile for producing a pseudo spot pattern representing matched and unmatched spots.

21. A method of matching protein spot patterns in a plurality of two-dimensional gel electrophoretograms, as recited in claim 16, wherein:

said step of comparing includes the step of verifying that potentially matching unknown spots are within an acceptable vector area formed by marker spot vectors before producing said matching results;

said producing matching results includes generating a single reference gel based matching spot datafile and generating a multiple reference gel based matching spot datafile having contradictory spot matching data and resolving said contradiction and producing a composite matching spot datafile; and

comparing said single reference gel based matching spot datafile with said multiple reference gel based datafile and further generating a potential mis-matched spot members datafile and a potential matched spot members datafile for improving accuracy of said spot matching results.

22. A method of matching two-dimensional (2-D) patterns, said method comprising the steps of:

(a) image scanning a plurality of 2-D patterns and producing corresponding data files for each scanned 2-D

pattern and recording logistic data and pattern physical characteristics data in a scan coordinate system;

(b) identifying pattern members in each of said scanned 2-D pattern that bound investigative patterns and designating said identified pattern members as marker members;

(c) designating one of said plurality of 2-D pattern as a reference 2-D pattern, said reference 2-D pattern having a reference pattern member data file which includes a set of reference marker members and unknown reference pattern members each having respective coordinates in said scan coordinate system;

(d) designating at least one of remaining ones of said plurality of 2-D patterns as a study 2-D pattern, said study 2-D pattern having a study pattern data file which includes a set of study marker members and unknown study pattern members each having respective coordinates in said scan coordinate system;

(e) performing at least one transformation step that transforms positional coordinates of said plurality of 2-D patterns from said scan coordinate system to a reference coordinate system for minimizing 2-D pattern preparation related distortions;

(f) repeating said steps (d) and (e) on any remaining one of said plurality of 2-D pattern;

(h) comparing physical characteristics of all pattern members in said 2-D patterns that were manipulated in accordance with said steps (d) through (f), said comparing including verifying that potentially matching unknown spots are within an acceptable vector area formed by marker spot vectors before producing said matching results; and

(i) producing matching results.

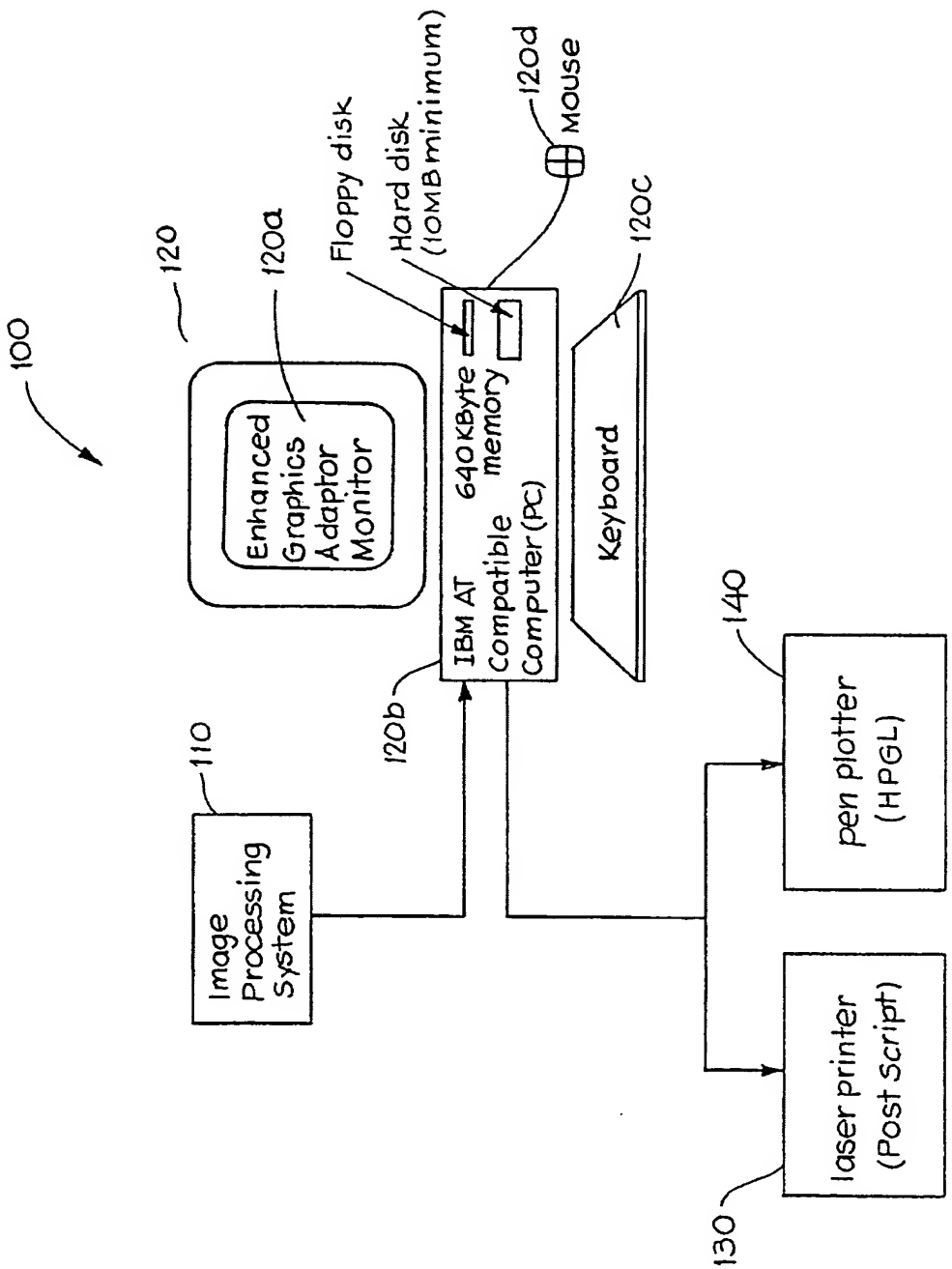
100
120
120a
Enhanced Graphics Adaptor Monitor
Floppy disk
Hard disk (10MB minimum)
120d
Mouse
120c
Keyboard
640 KByte memory
IBM AT Compatible Computer (PC)
120b
110
Image Processing System
140
pen plotter (HPGL)
130
laser printer (Post Script)

FIG. 1

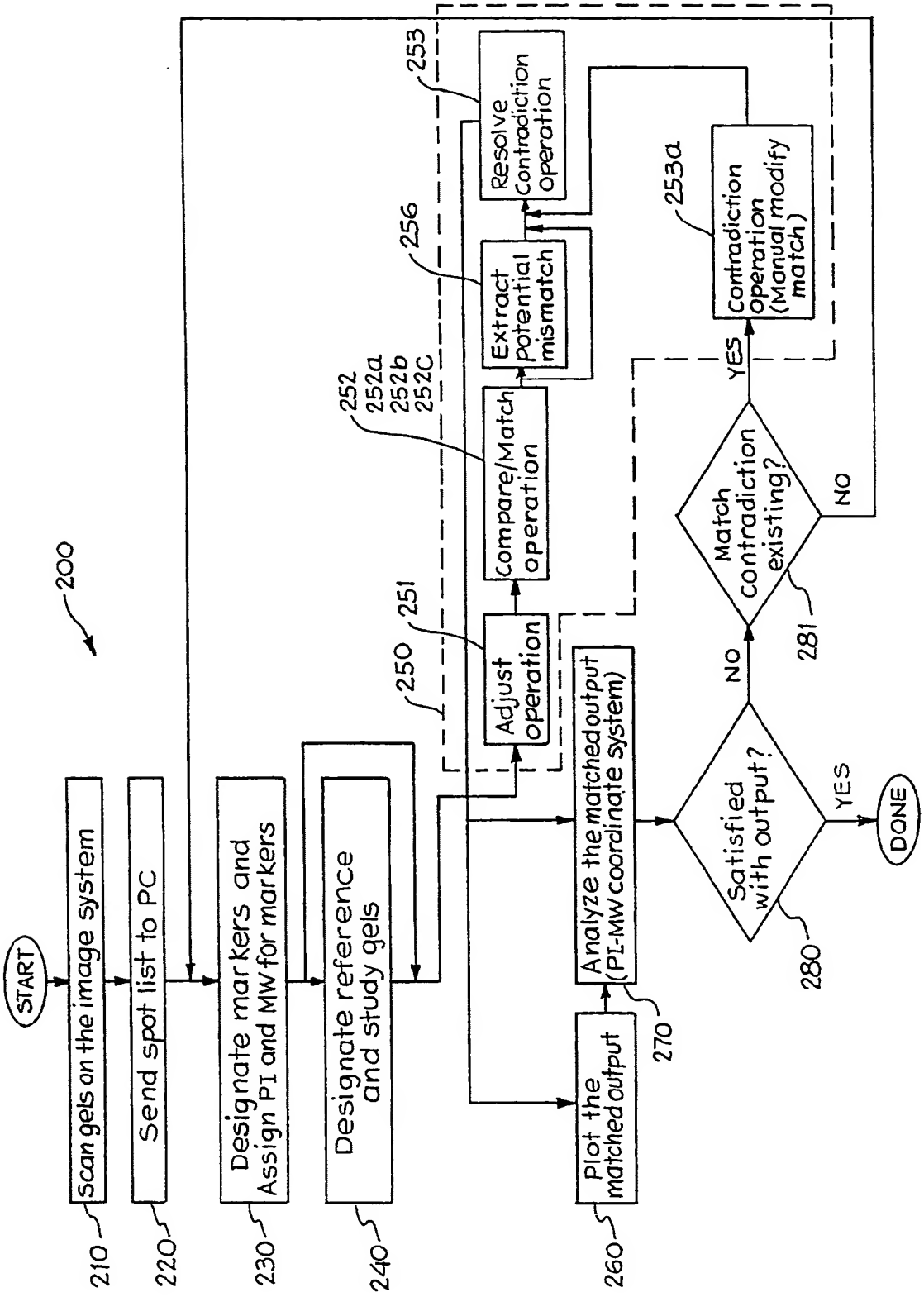
200
START
Scan gels on the image system
210
Send spot list to PC
220
Designate markers and Assign PI and MW for markers
230
Designate reference and study gels
240
250
251
Adjust operation
252
252a
252b
252c
Compare/Match operation
253
Resolve Contradiction operation
256
Extract potential mismatch
Plot the matched output
260
270
Analyze the matched output (PI-MW coordinate system)
Satisfied with output?
280
NO
YES
DONE
Match contradiction existing?
281
NO
YES
253a
Contradiction operation (Manual modify match)

FIG. 2

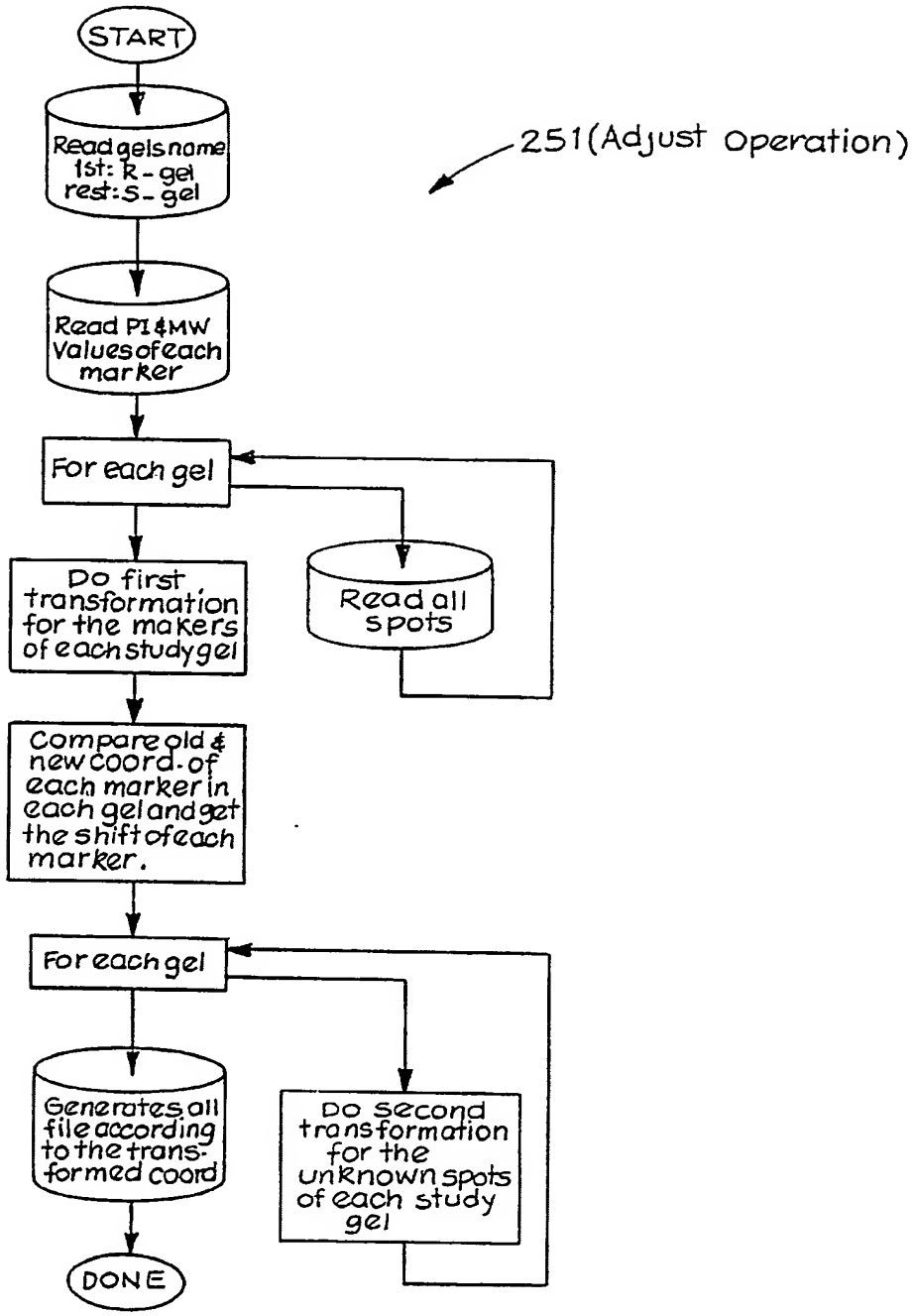
START
Read gels name 1st: R-gel rest: S-gel
251(Adjust Operation)
Read PI & MW Values of each marker
For each gel
Do first transformation for the makers of each study gel
Read all spots
Compare old & new coord. of each marker in each gel and get the shift of each marker.
For each gel
Generates all file according to the trans-formed coord
Do second transformation for the unknown spots of each study gel
DONE

FIG. 2a

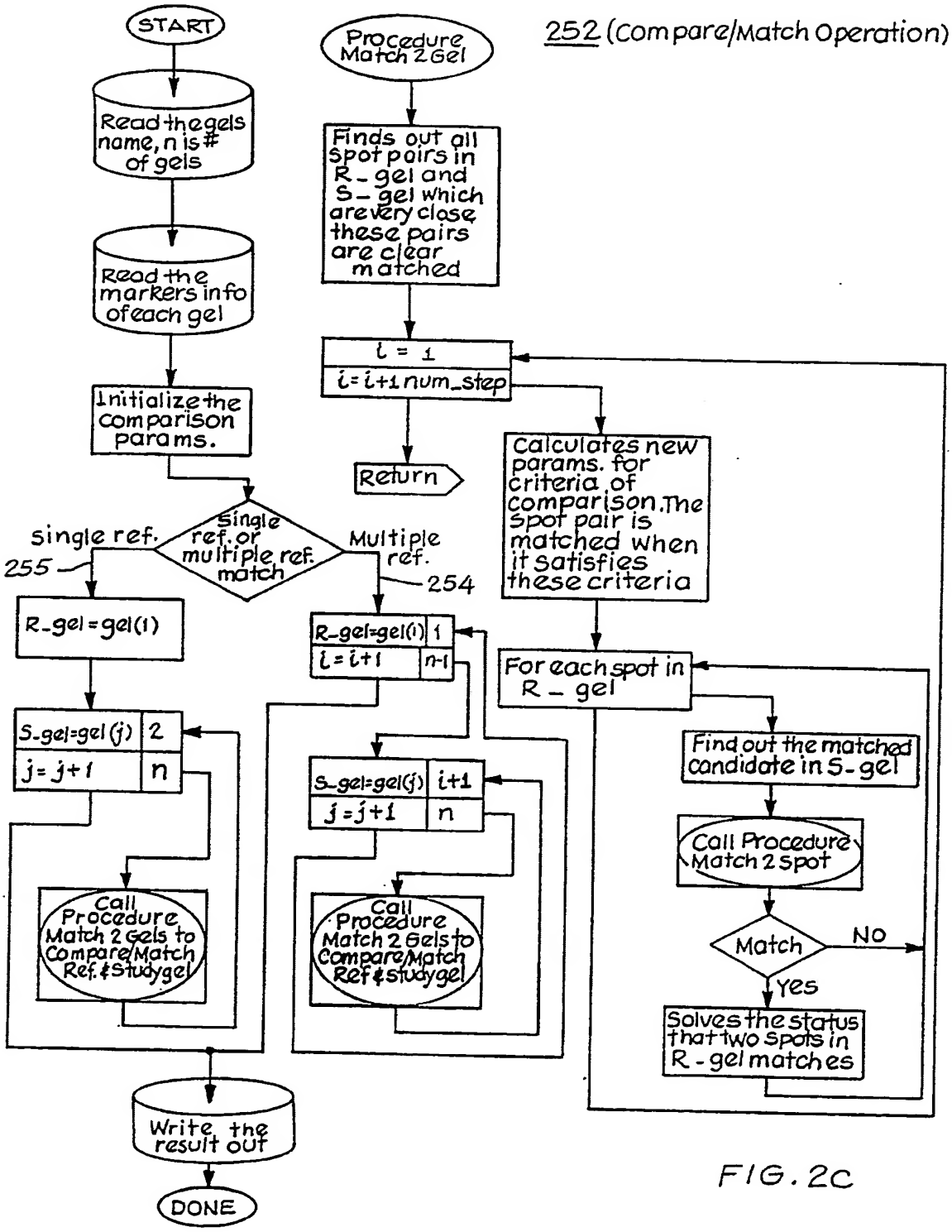
START
Read the gels name, n is # of gels
Read the markers info of each gel
Initialize the comparison params.
Single ref. or multiple ref. match
single ref.
255
Multiple ref.
254
R_gel = gel(1)
S_gel=gel(j) 2
j = j+1 n
Call Procedure Match 2 Gels to Compare/Match Ref. & Study gel
R_gel=gel(i) 1
i = i+1 n-1
S_gel=gel(j) i+1
j = j+1 n
Call Procedure Match 2 Gels to Compare/Match Ref & study gel
Write the result out
DONE
Procedure Match 2 Gel
Finds out all spot pairs in R_gel and S_gel which are very close these pairs are clear matched
i = 1
i = i+1 num_step
Return
Calculates new params. for criteria of comparison. The spot pair is matched when it satisfies these criteria
For each spot in R_gel
Find out the matched candidate in S_gel
Call Procedure Match 2 Spot
Match
No
Yes
Solves the status that two spots in R_gel matches
252 (Compare/Match Operation)

FIG. 2b

FIG. 2c

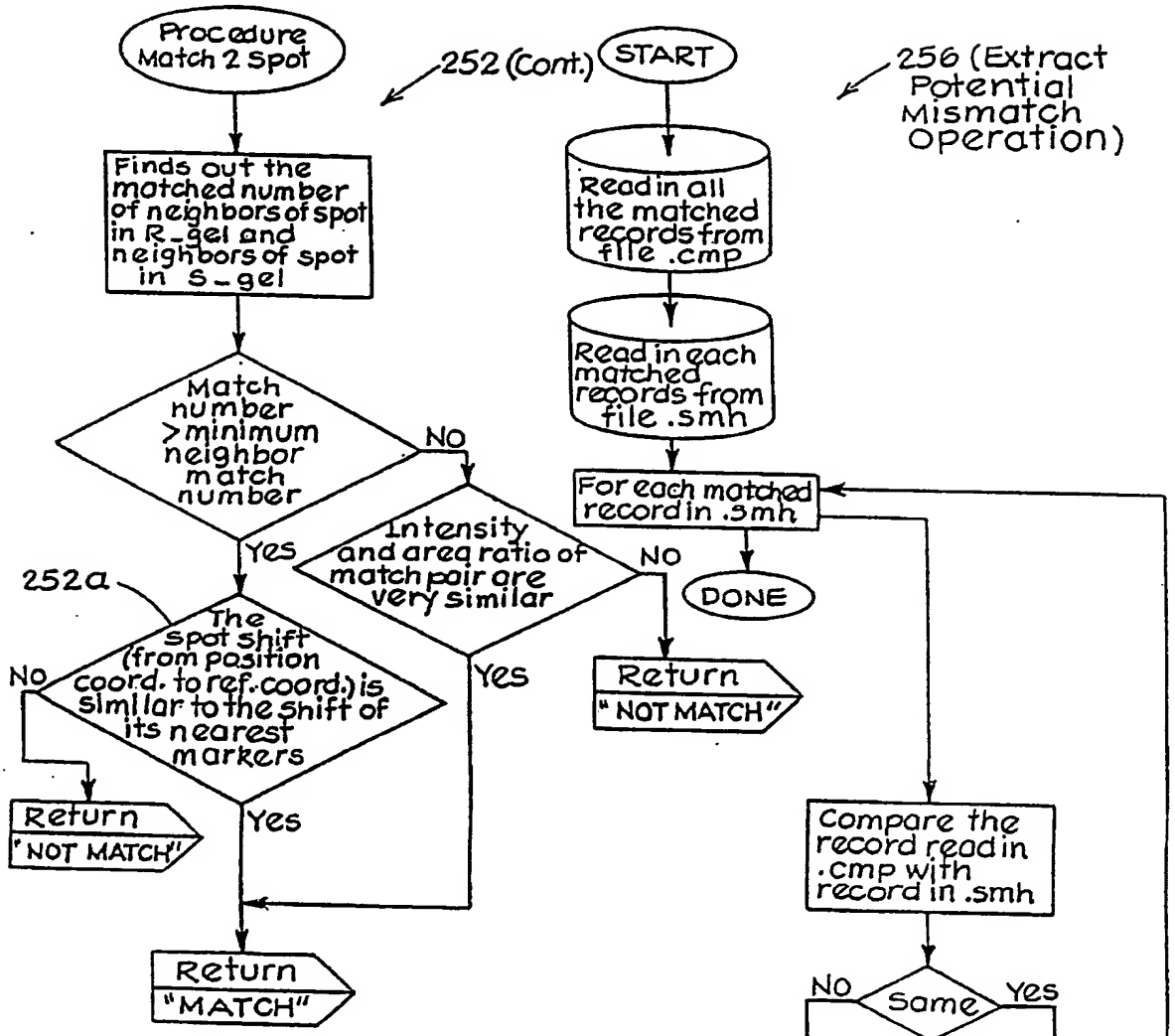
Procedure Match 2 Spot
Finds out the matched number of neighbors of spot in R_gel and neighbors of spot in S_gel
Match number > minimum neighbor match number
NO
Yes
252a
The spot shift (from position coord. to ref. coord.) is similar to the shift of its nearest markers
No
Return "NOT MATCH"
Yes
Return "MATCH"
252 (Cont.)
START
Read in all the matched records from file .cmp
Read in each matched records from file .smh
For each matched record in .smh
Intensity and area ratio of match pair are very similar
NO
DONE
Yes
Return "NOT MATCH"
256 (Extract Potential Mismatch operation)
Compare the record read in .cmp with record in .smh
Same
No
Yes
Write the record which read in .smh to file .pmm
Write the record which read in .smh to file .pcm

FIG. 2d

FIG. 2e

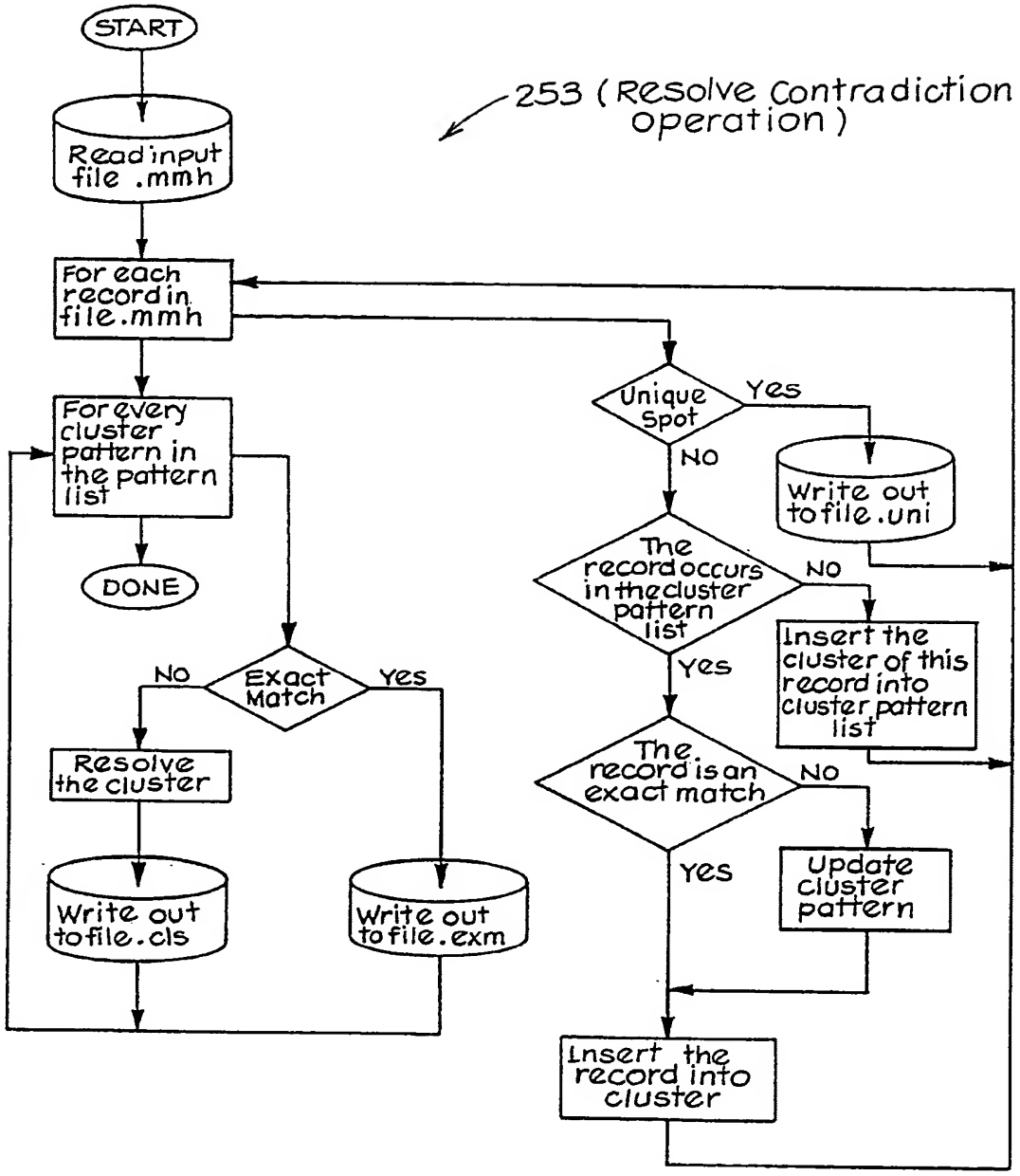
START
Read input file .mmh
For each record in file.mmh
For every cluster pattern in the pattern list
DONE
Exact Match
NO
YES
Resolve the cluster
Write out to file.cls
Write out to file.exm
253 (Resolve Contradiction operation)
Unique Spot
YES
NO
Write out to file.uni
The record occurs in the cluster pattern list
NO
YES
Insert the cluster of this record into cluster pattern list
The record is an exact match
NO
YES
Update cluster pattern
Insert the record into cluster

FIG. 2f

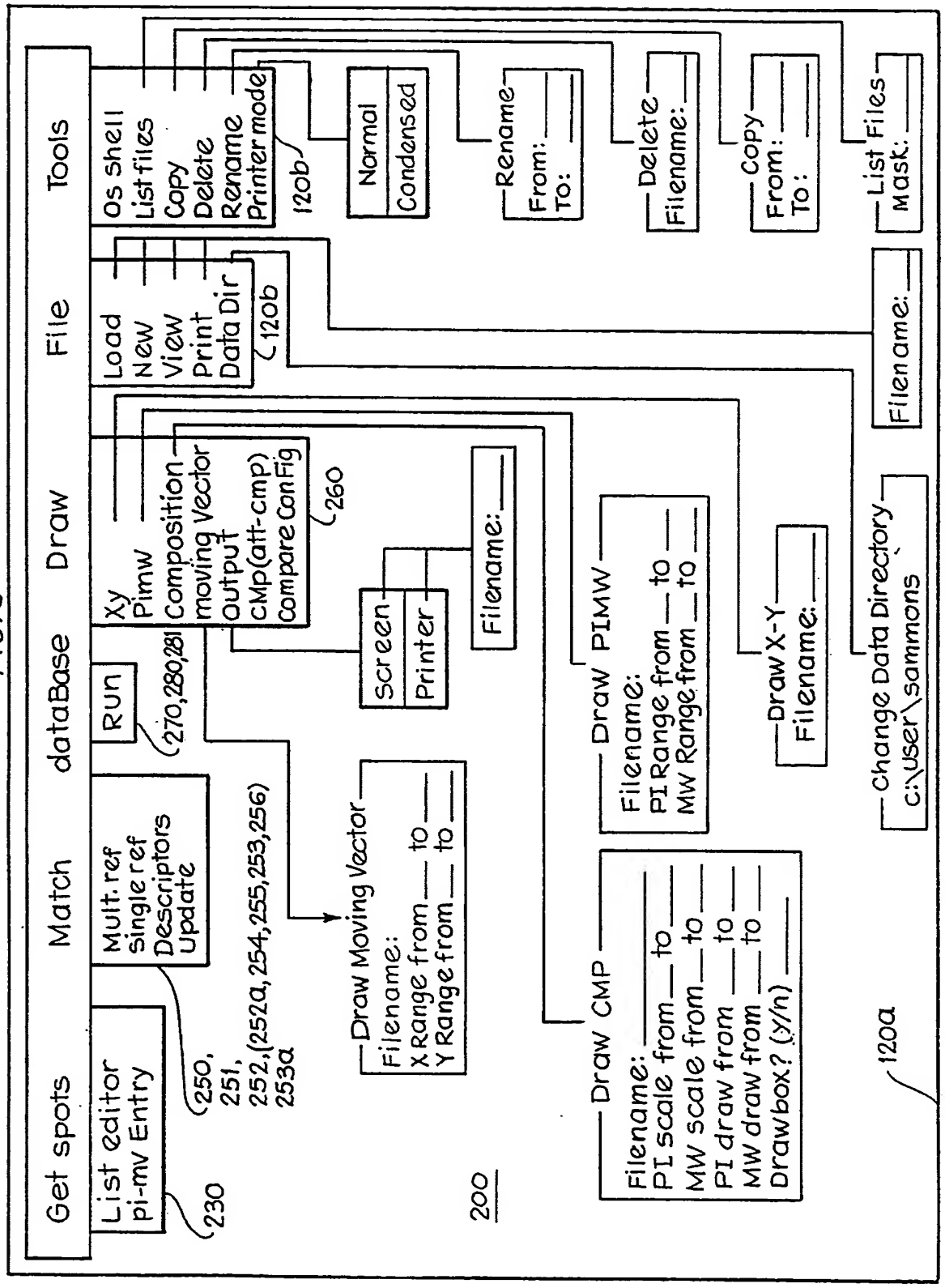
Get spots
Match
dataBase
Draw
File
Tools
List editor pi-mv Entry
Mult. ref single ref Descriptors Update
Run
Xy
Pimw
Composition
moving Vector
output
CMP(att-cmp)
compare conFig
Load
New
View
Print
Data Dir
Os shell
List files
Copy
Delete
Rename
Printer mode
Normal
Condensed
Rename
From:
To:
Delete
Filename:
Copy
From:
To:
List Files
Mask:
Filename:
Change Data Directory
c:\user\sammons
Draw Moving Vector
Filename:
X Range from ___ to ___
Y Range from ___ to ___
Screen
Printer
Filename:
Draw CMP
Filename:
PI scale from ___ to ___
MW scale from ___ to ___
PI draw from ___ to ___
MW draw from ___ to ___
Draw box? (y/n) ___
Draw PIMW
Filename:
PI Range from ___ to ___
MW Range from ___ to ___
Draw X-Y
Filename:
270,280,281
250,
251,
252,(252a, 254,255,253,256)
253a
260
230
120b
120b
120a
200

FIG. 3

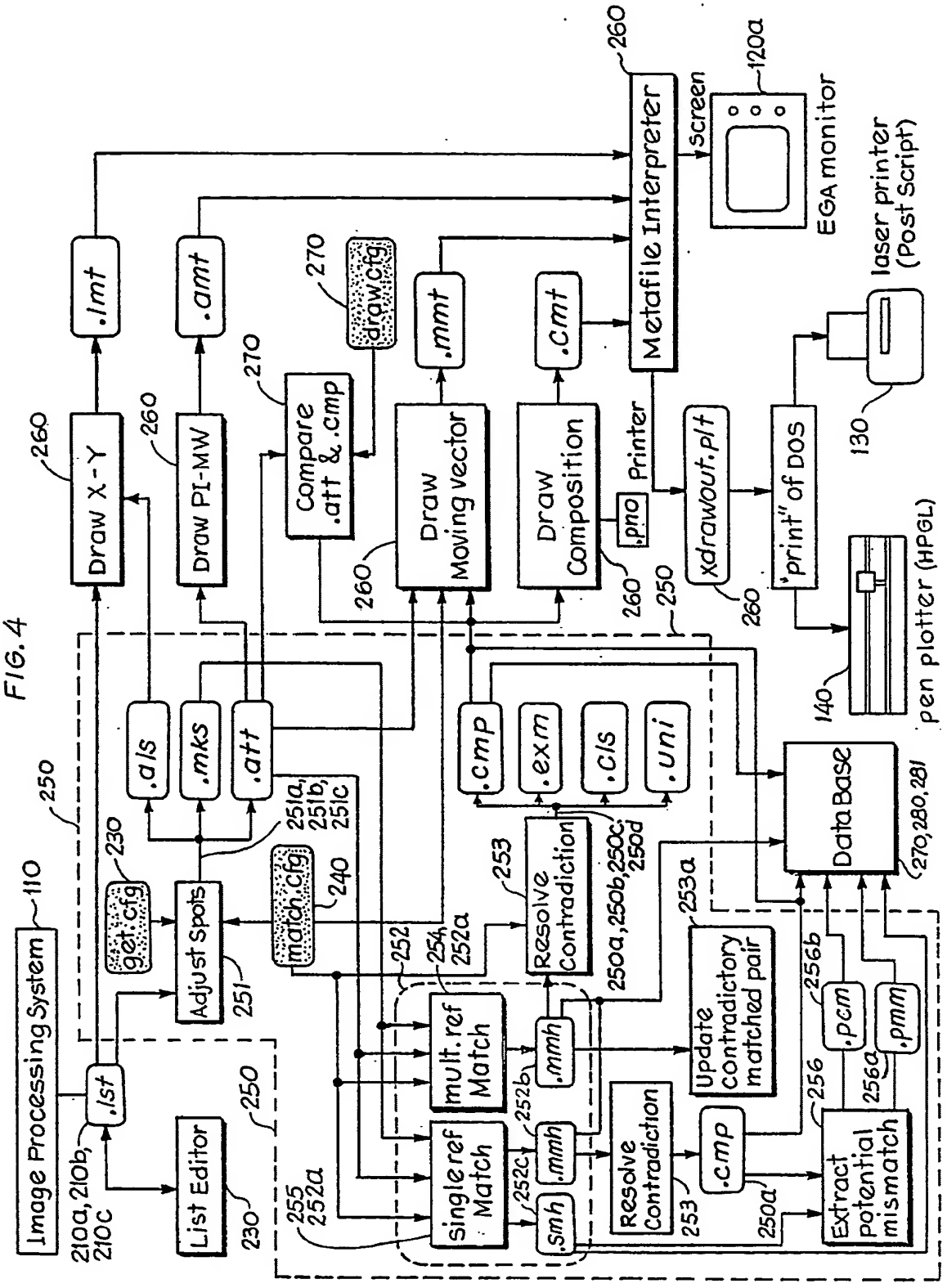
Image Processing System
110
210a, 210b, 210c
.lst
List Editor
230
250
get.cfg
230
Adjust Spots
251
match.cfg
240
2510, 251b, 251c
252
254
252a
.als
.mks
.att
Draw X-Y
Draw PI-MW
.lmt
.amt
260
270
Compare .att & .cmp
draw.cfg
Draw Moving vector
Draw Composition
.mmt
.cmt
.cmp
.exm
.cls
.uni
Metafile Interpreter
Screen
EGA monitor
120a
laser printer (Post Script)
130
Printer
.pmo
xdrawout.plt
"print" of DOS
pen plotter (HPGL)
140
Data Base
270, 280, 281
Resolve Contradiction
253
250a, 250b, 250c, 250d
253a
Update contradictory matched pair
mult. ref Match
.mmh
singleref Match
.smh
252b
252c
255
252a
Resolve contradiction
.cmp
250a
Extract potential mismatch
256
256a
.pmm
256b
.pcm

FIG. 4

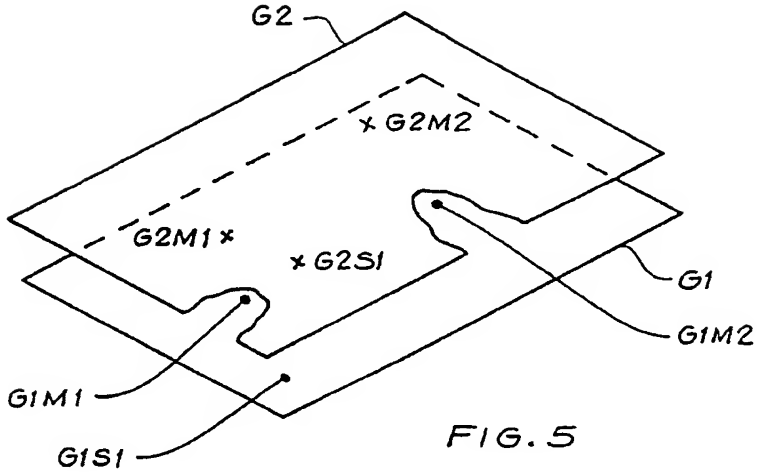

FIG. 5

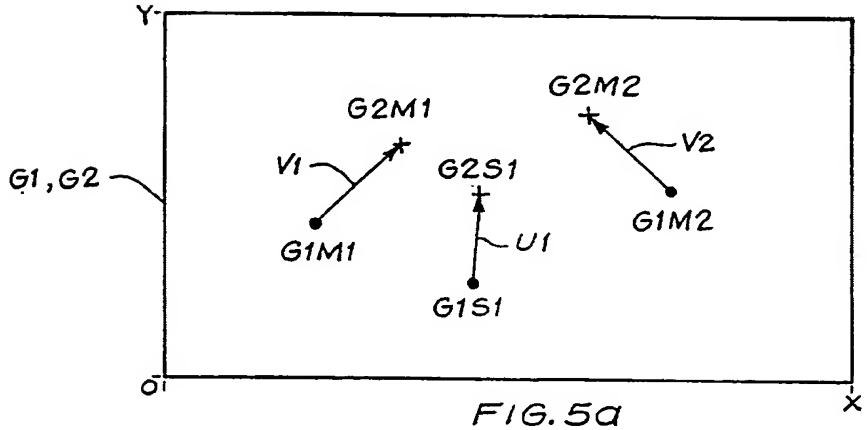

FIG. 5a

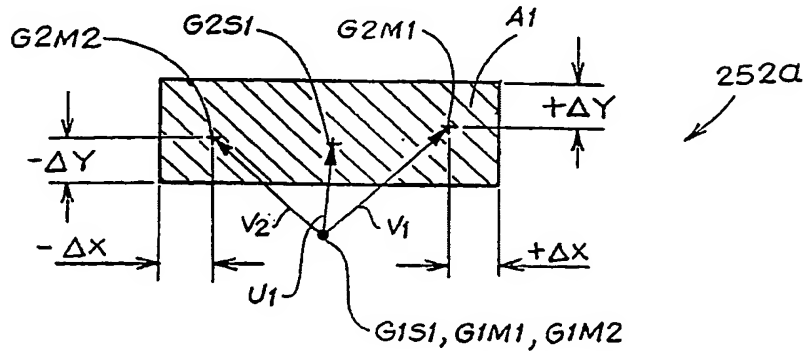

FIG. 5b

INTERNATIONAL SEARCH REPORT

International Application No. PCT/US91/03620

I. CLASSIFICATION OF SUBJECT MATTER (if several classification symbols apply, indicate all) [6]

According to International Patent Classification (IPC) or to both National Classification and IPC

IPC(5): G06K 9/62, G06K 15/00 G06K 9/00

US CL : 382/6,30,44; 358/111 364/413.13, 413.01

II. FIELDS SEARCHED

Minimum Documentation Searched [7]

Classification System	Classification Symbols
US	382/6,30,44; 364/413.13, 413.01 358/111

Documentation Searched other than Minimum Documentation to the Extent that such Documents are Included in the Fields Searched [8]

III. DOCUMENTS CONSIDERED TO BE RELEVANT [9]

Category *	Citation of Document, [11] with indication, where appropriate, of the relevant passages [12]	Relevant to Claim No. [13]
A	US,A 4,894,786 (HARA) 16 January 1990, See Fig. 9	
A	US,A 4,644,582 (MORISHITA et al) 17 February 1987, See Figs. 1-19	
A,P	US,A 4,956,872 (KIMURA) 11 September 1990, See abstract	
A	US,A 4,825,388 (DAILEY et al) 25 April 1989, See abstract	
A	US,A 4,618,937 (ELIS et al) 21 October 1986, See Figs 1-6	
A	US,A 4,741,043 (BACUS) 26 April 1988 See abstract and Fig. 1.	

* Special categories of cited documents: [10]

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

IV. CERTIFICATION

Date of the Actual Completion of the International Search	Date of Mailing of this International Search Report
20 August 1991	09 SEP 1991
International Searching Authority	**Signature of Authorized Officer**
ISA/US	Michael Razavi

Form PCT/ISA/210 (second sheet) (Rev.11-87)